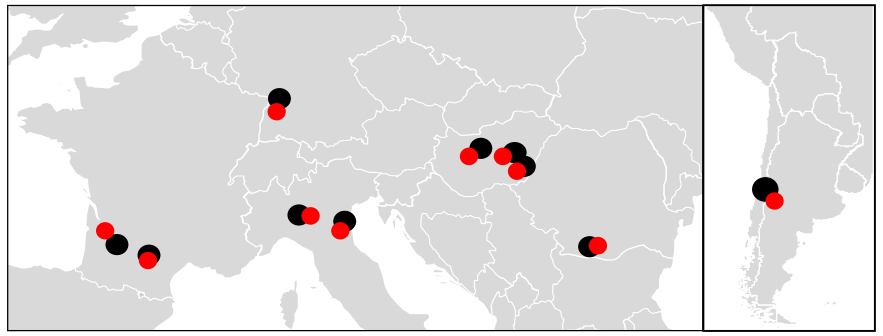
How can we learn from plant breeders?
Update on use of digital technologies in plant breeding.

F. Tardieu



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Laboratoire d'Ecophysiologie des Plantes sous Stress Environnementaux
lepse
Montpellier

PHENOME
FRANCE EMPHASIS

European
Plant Phenotyping
Network
EPPN 2020

DROPS
amaizing

What is breeder’s demand for phenotyping ?

A false evidence: phenotyping for traits is essential for breeding
BUT selection programs are based on yield (genomic selection) not on traits

Richard and Sadras 2014 J Exp Bot

- *‘The limited success of indirect selection to improve crop yield’*
- *‘Indirect methods, based on secondary traits (…) a complement to direct selection for yield’*

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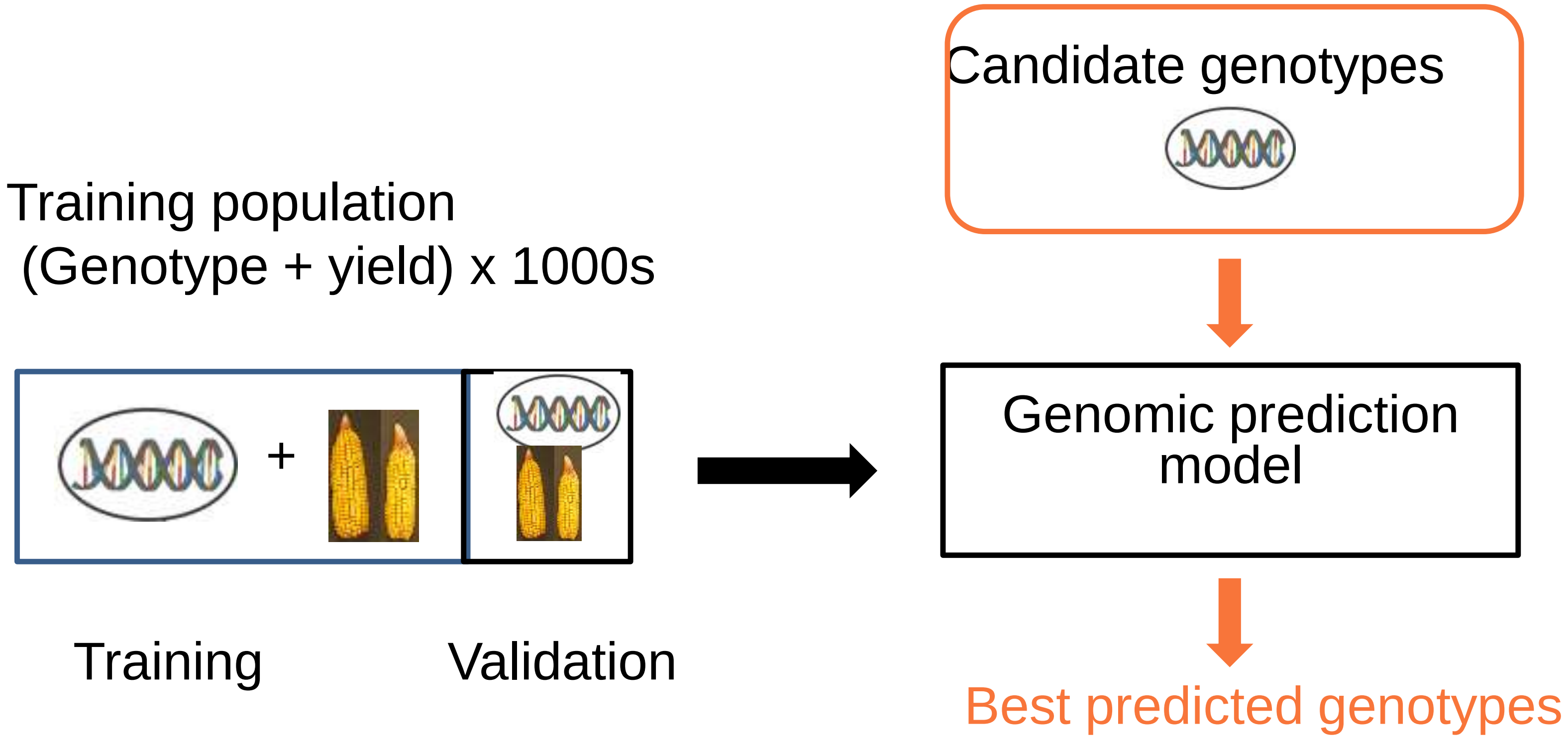
Genomic selection for yield

1. Yield in large network of fields
2. Genomic prediction : which combinations of alleles are most promising (from genome only)



Candidate genotypes

Training population
(Genotype + yield) x 1000s

+

Genomic prediction model

Training

Validation

Best predicted genotypes

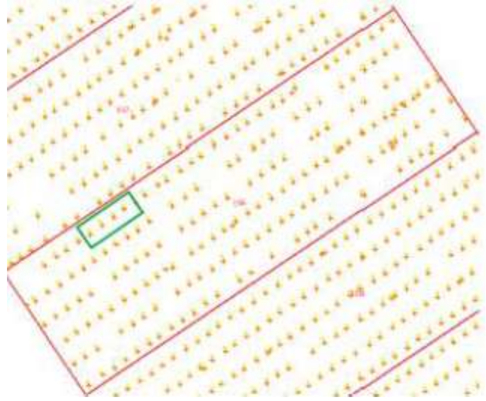
3. Test of most promising genotypes in networks of fields

What is breeder’s demand for phenotyping ?

Selection is essentially on yield, based on genomic prediction: heavy machinery

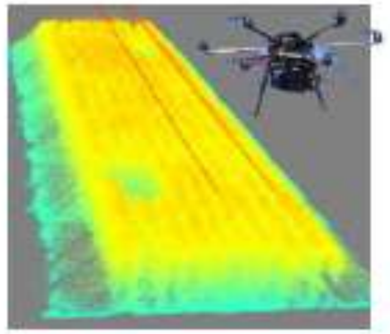
Current demand for phenotyping: co-variables for genomic prediction model
Prediction for logistics

- Final plant number in each microplot: exclude some microplots or correct them



(drone + image analysis)

- Prediction of yield and date few weeks before harvest



: optimize the process in factories (seeds, vegetables)
(drone + machine learning)

What is breeder’s demand for phenotyping ?

Selection is essentially on yield, based on genomic prediction: heavy machinery

Current demand for phenotyping: co-variables for genomic prediction model
yield prediction for logistics

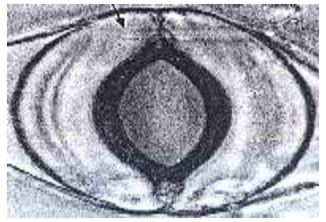
No major demand from breeders for the genetic variability of physiological traits

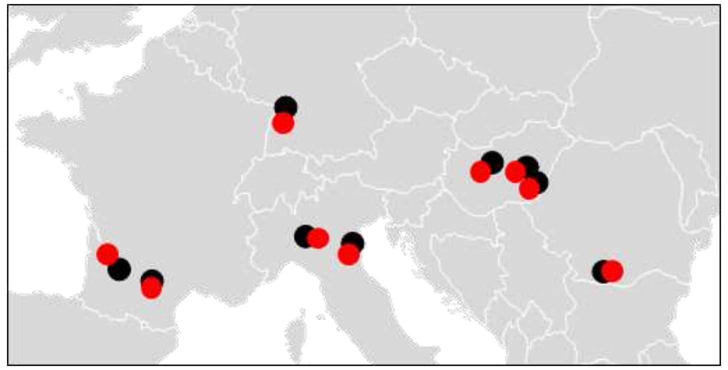
BUT Some traits still taken into account
- *Duration of plant cycle*
- *Disease resistance*

(end of this presentation)

Why a low demand for phenotyping in breeding

Scale	Cell- cm^2 Minutes / days	Organ(s) Minute/days	Plant or Canopy Minute to weeks	Multi-environment field network Weeks to months
	'Physiology community'	*'FSPM community'*		*'Crop models community'*





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Physiological traits defined over minutes, yield over months				

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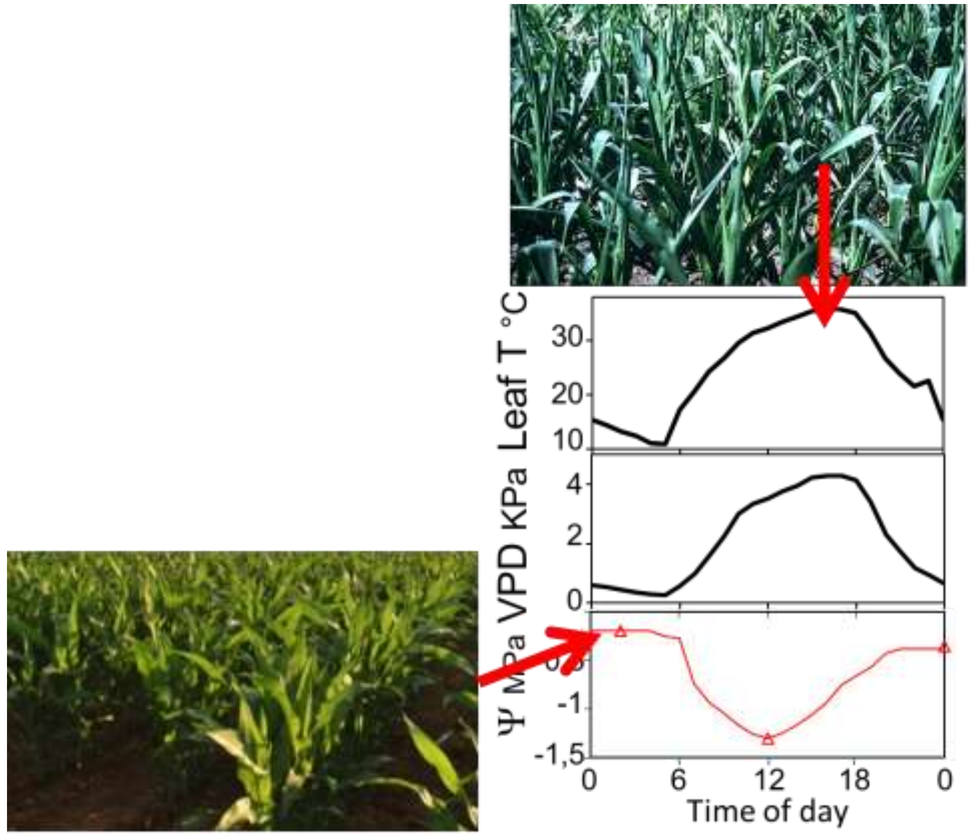
Environmental variations are everywhere, between minutes and between years



Tardieu et al 2017 Current Biology.

“Tell me the date and minute, I’ll give you the trait value”

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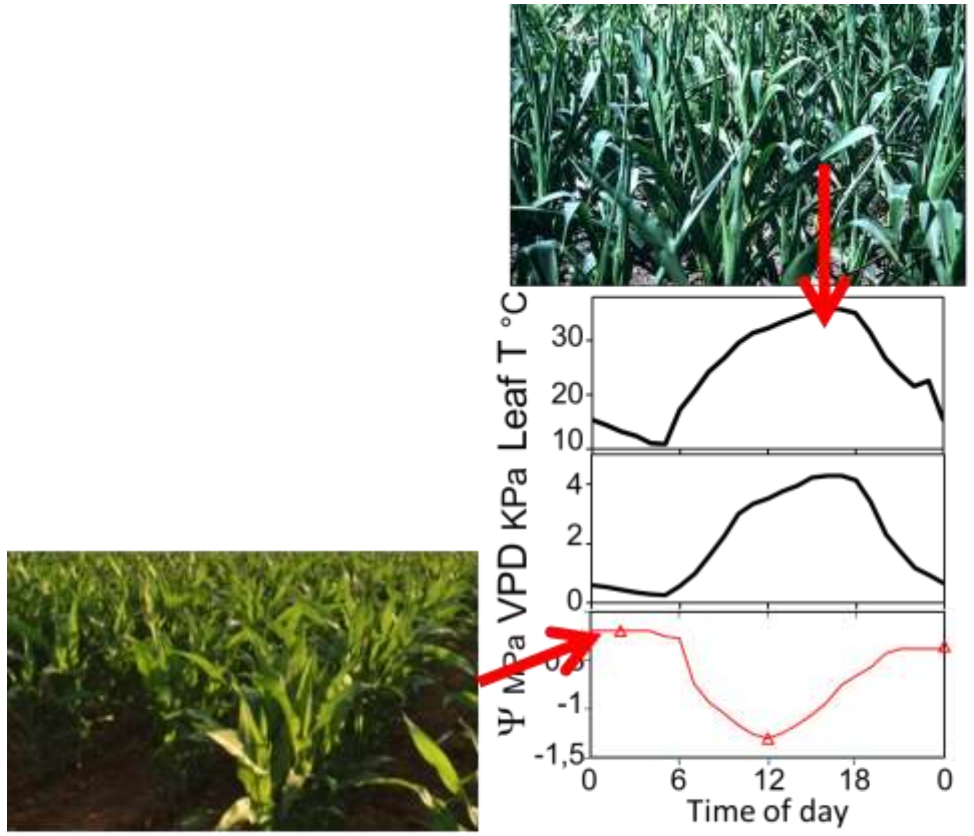

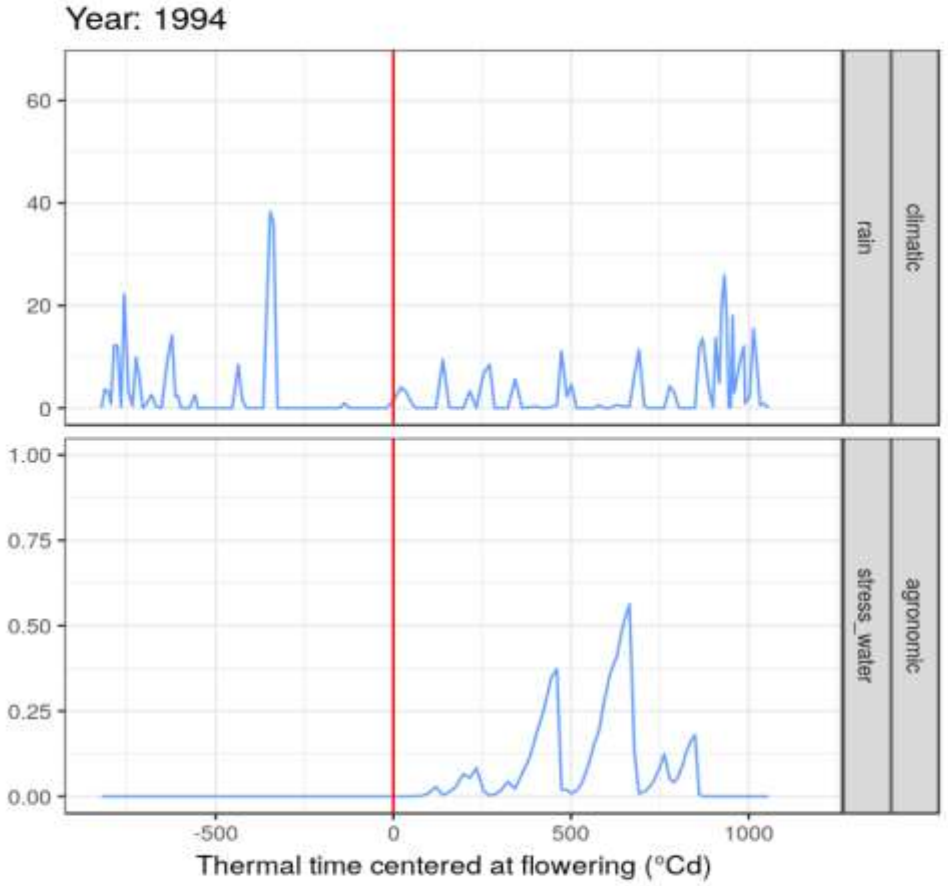

Tardieu et al 2017 Current Biology.

Casadebaig P 2016 EJA

"Tell me the date and minute, I'll give you the trait value ; Tell me the year, I'll give you the yield value"

Genetic progress in maize, 1950 - 2010

Breeders successfully “avoided” the problem: large networks of fields + yield-based genomic selection

What did breeders reach by selecting for yield ?

➔*Progress in ‘tolerance’ ?*

➔*Which traits were (indirectly) selected ?*

➔ *Margin for progress ?*

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➔ *Margin for progress ?*

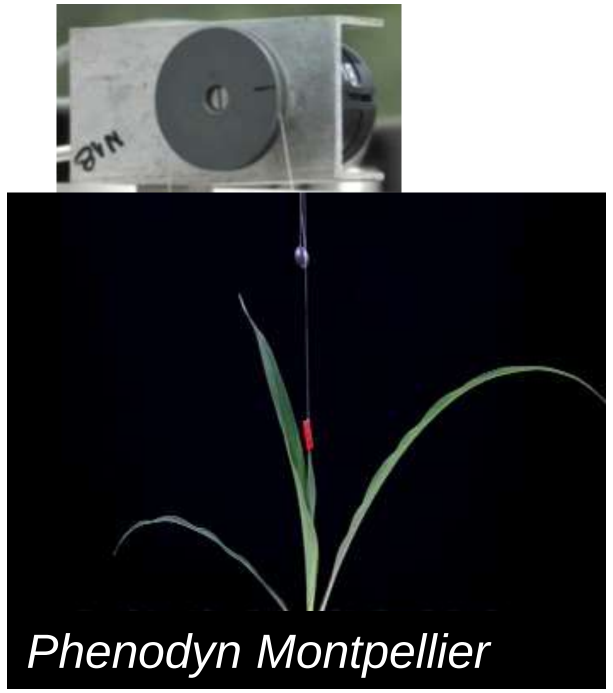

PhenoArch Montpellier

A panel of 64 most successful European hybrids
- Yield in 24 field experiments
- Traits in 10 detailed experiments in phenotyping platforms
  + 3 equipped fields


DiaPhen Montpellier

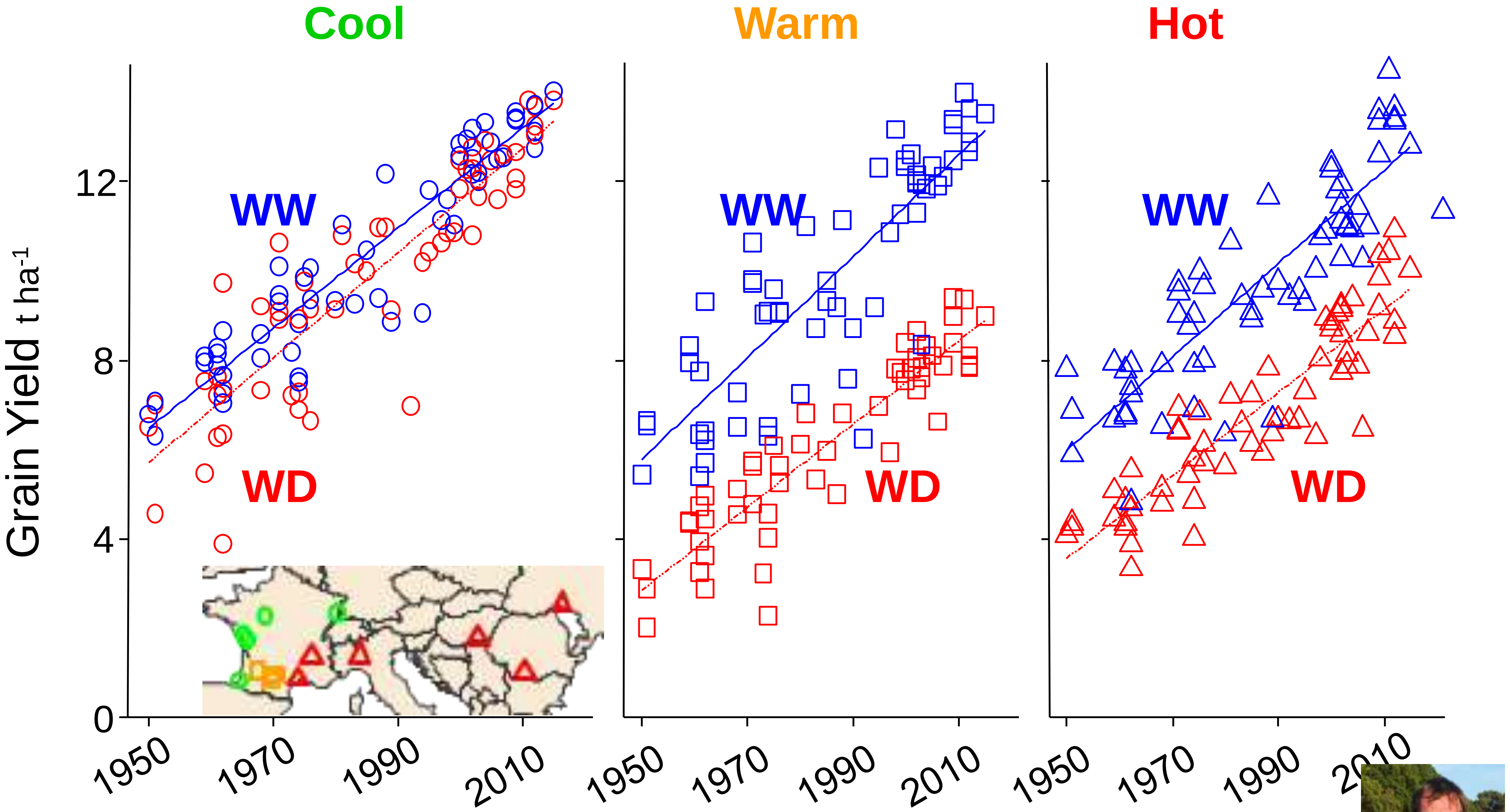

PhenoField Arvalis, Ouzouer


RootPHAIR, LLN


Phenodyn Montpellier

Genetic progress in maize, 1950 - 2010

Yield increased (+100 kg ha^{-1} y^{-1})
in all environmental scenarios



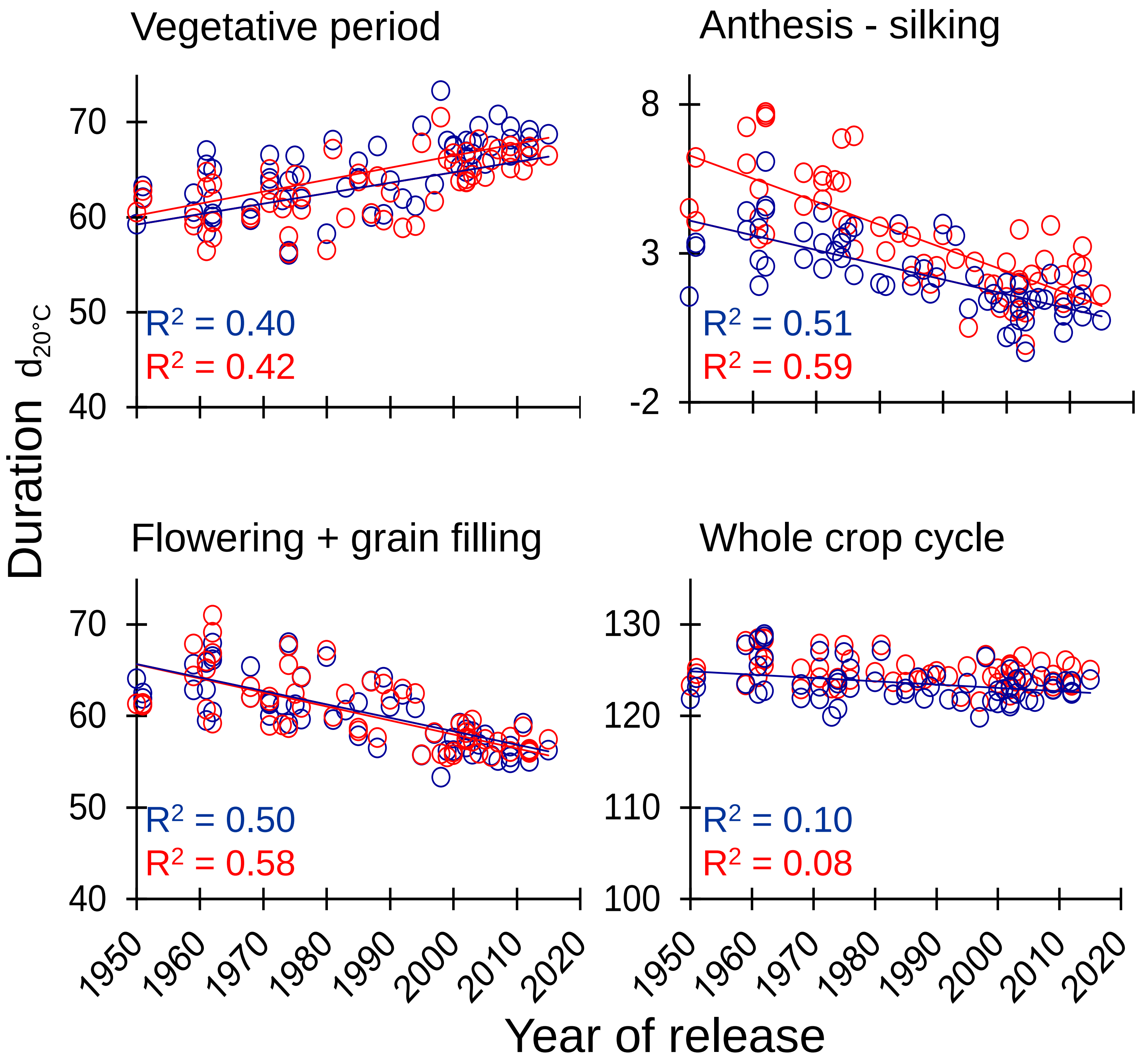
Welcker et al 2022, Nature Communications

C. Welcker

N Abou Amra
Spencer

Genetic progress in maize, 1950 – 2010 Phenology and reproductive development

The vegetative period increased with year of release at the expense of the grain filling period

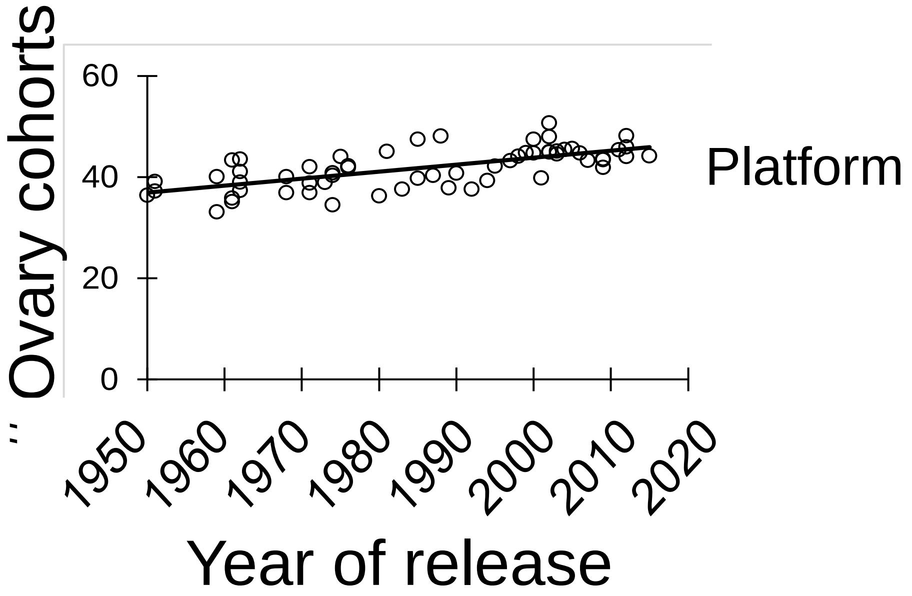


Welcker et al 2022, Nature Communications

Genetic progress in maize, 1950 – 2010 Phenology and reproductive development

Improved reproductive development

More time = more ovary cohorts



Welcker et al 2022, Nature Communications

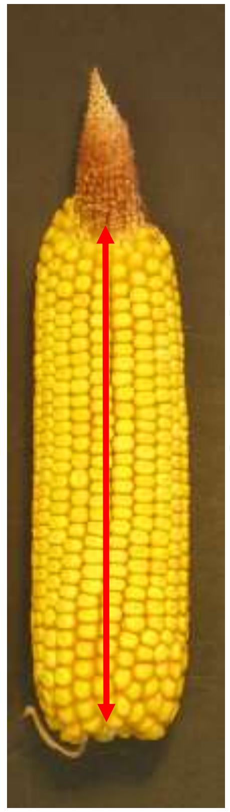
O. Turc

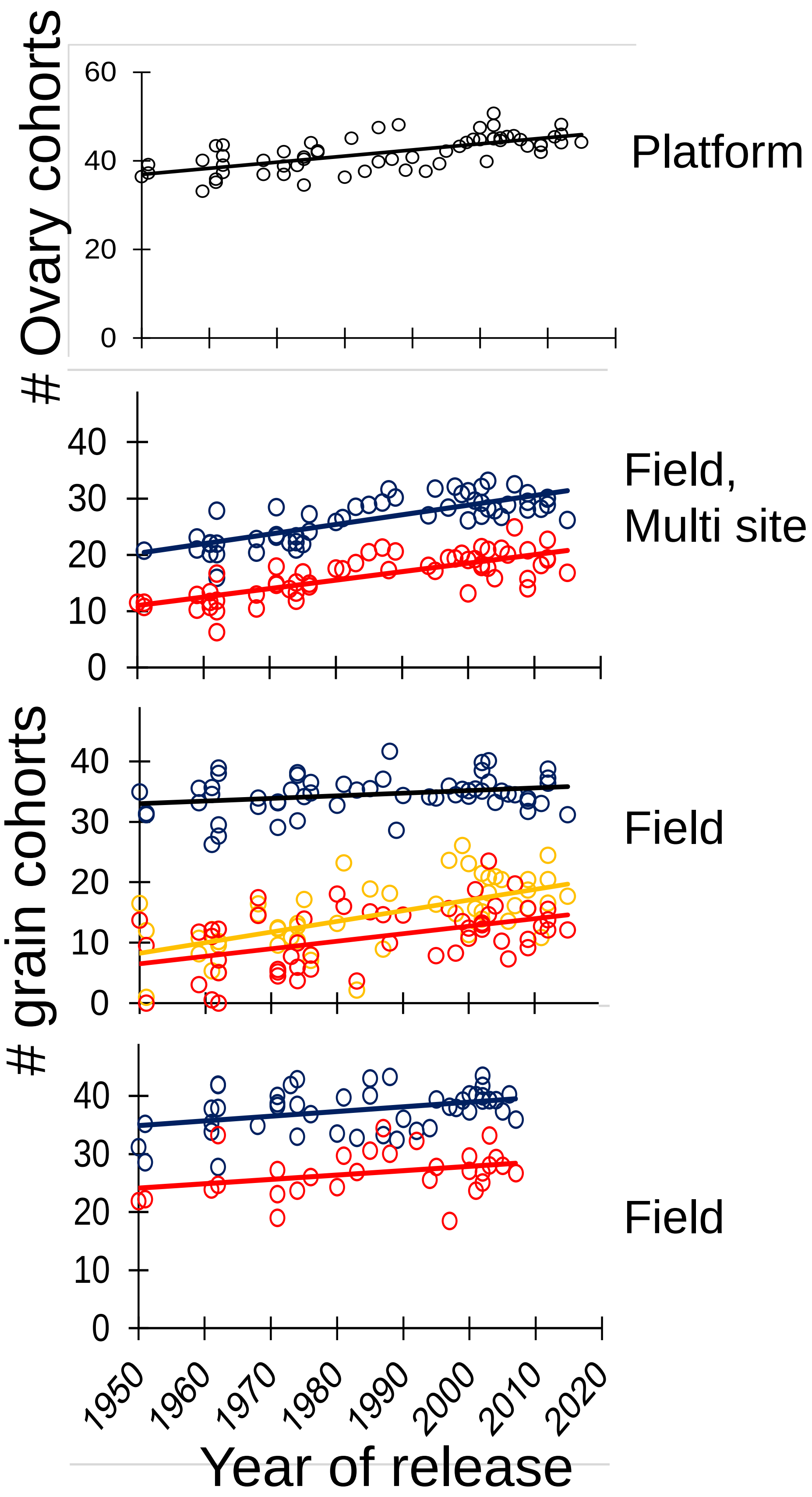
Genetic progress in maize, 1950 – 2010 Phenology and reproductive development

Improved reproductive development
More time = more ovary cohorts

Better silk growth in all conditions:
➔less abortion
➔(and indirectly decreased ASI)

➔ ***More grain cohorts***
in all environmental conditions

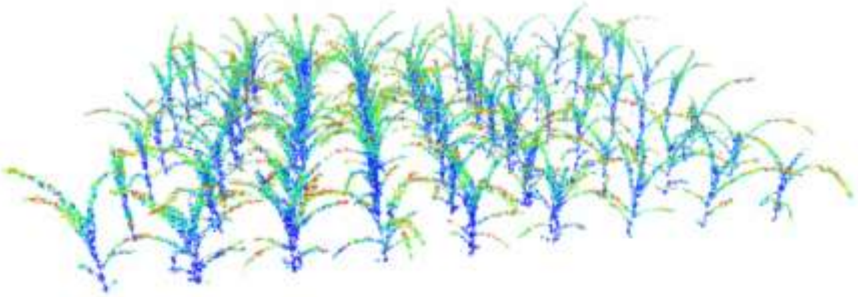




Welcker et al 2022, Nature Communications

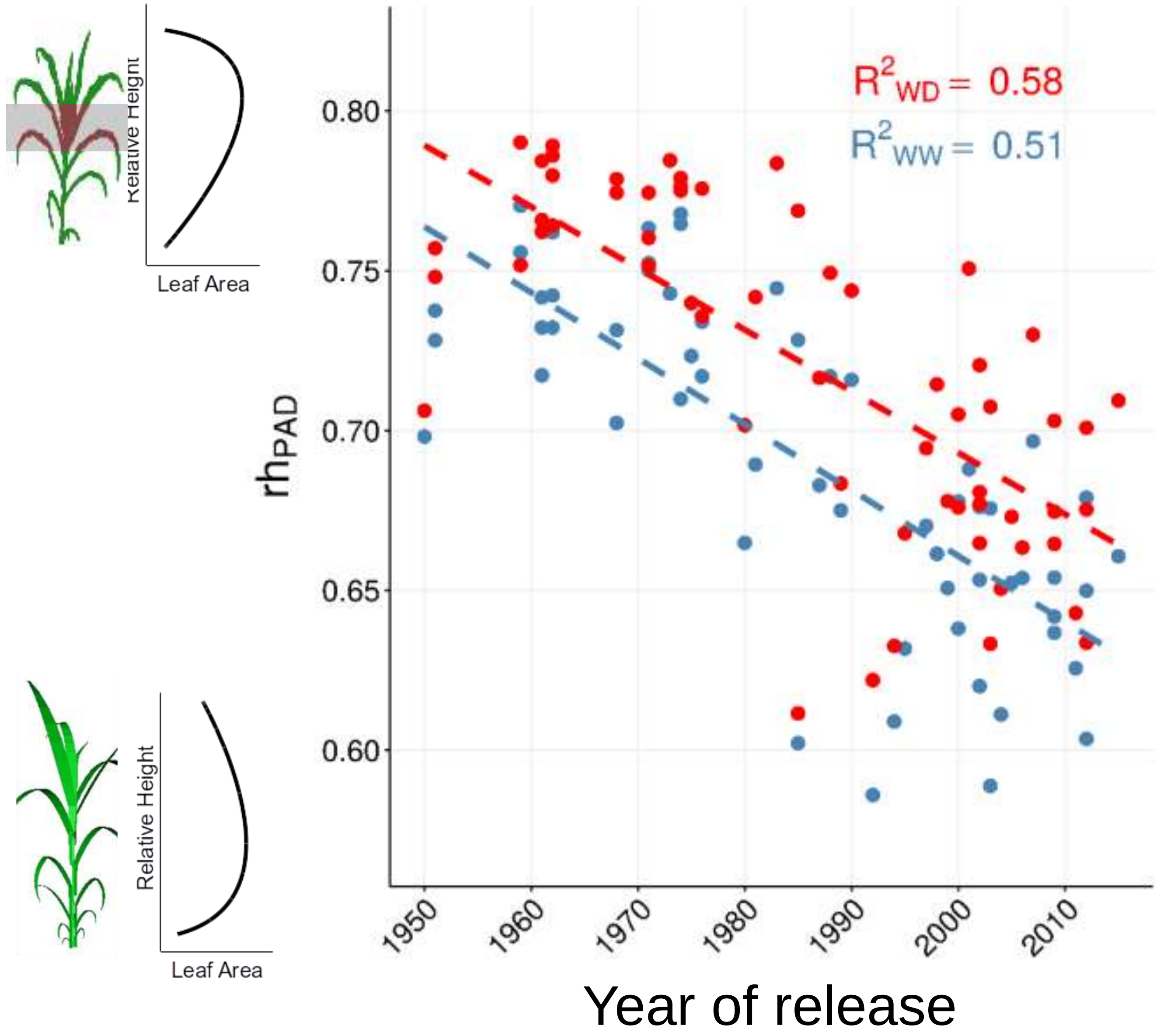
O. Turc

Genetic progress in maize, 1950 – 2010 Plant architecture and light interception



More efficient vertical distribution of leaf area

➔ Increased radiation use efficiency



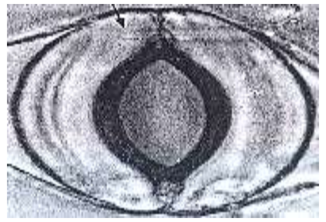
Same result in the ERA series

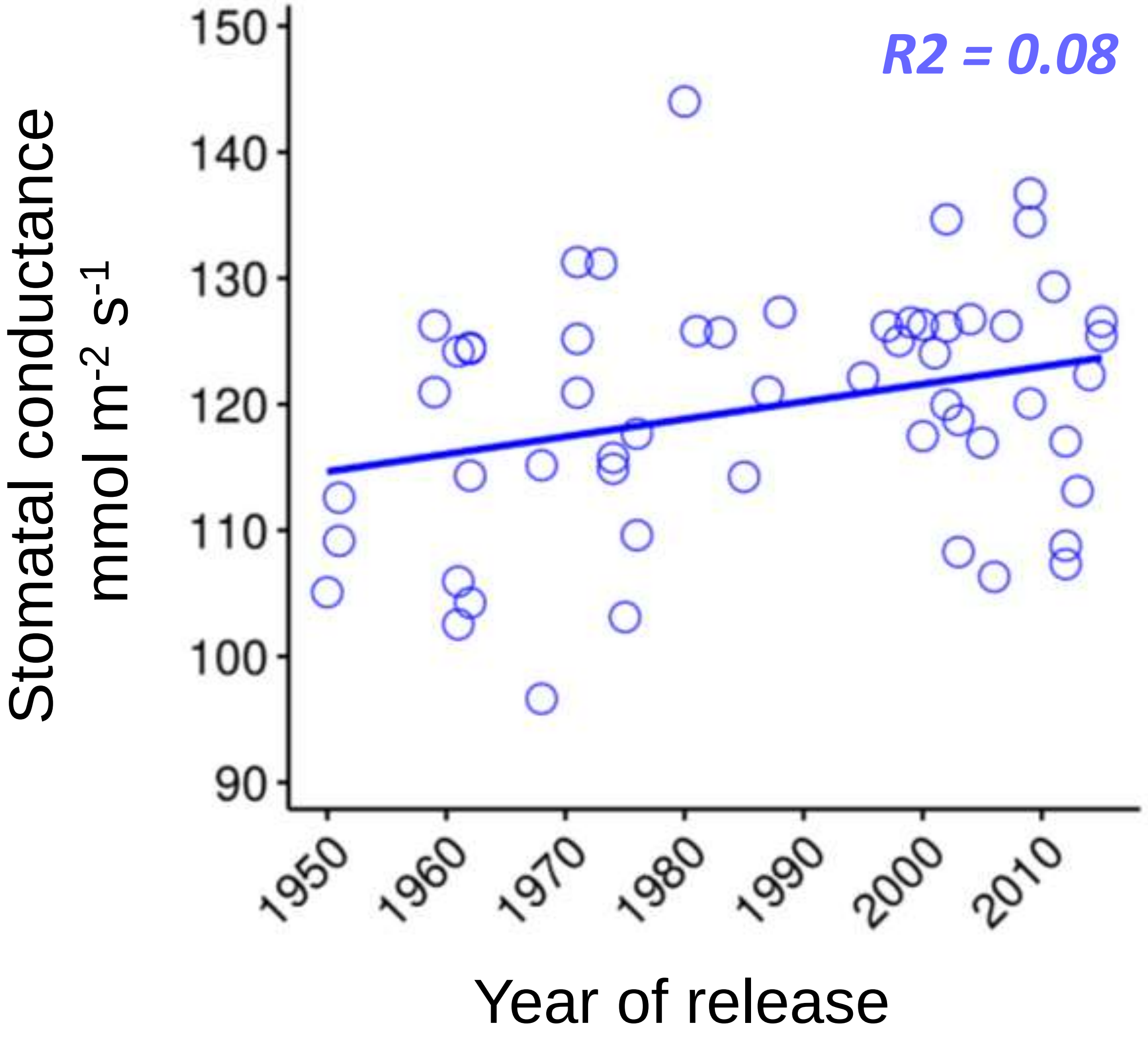
R. Perez *C Fournier*

Perez *et al.*, (2018), *Plant Cell Environ*

Genetic progress in maize, 1950 – 2010 Physiological adaptive processes

BUT stomatal conductance essentially unchanged





Ll Cabrera

N Abou Amra
Spencer

S. Alvarez
Prado

Welcker et al 2022, Nature Communications

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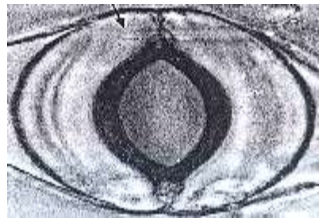
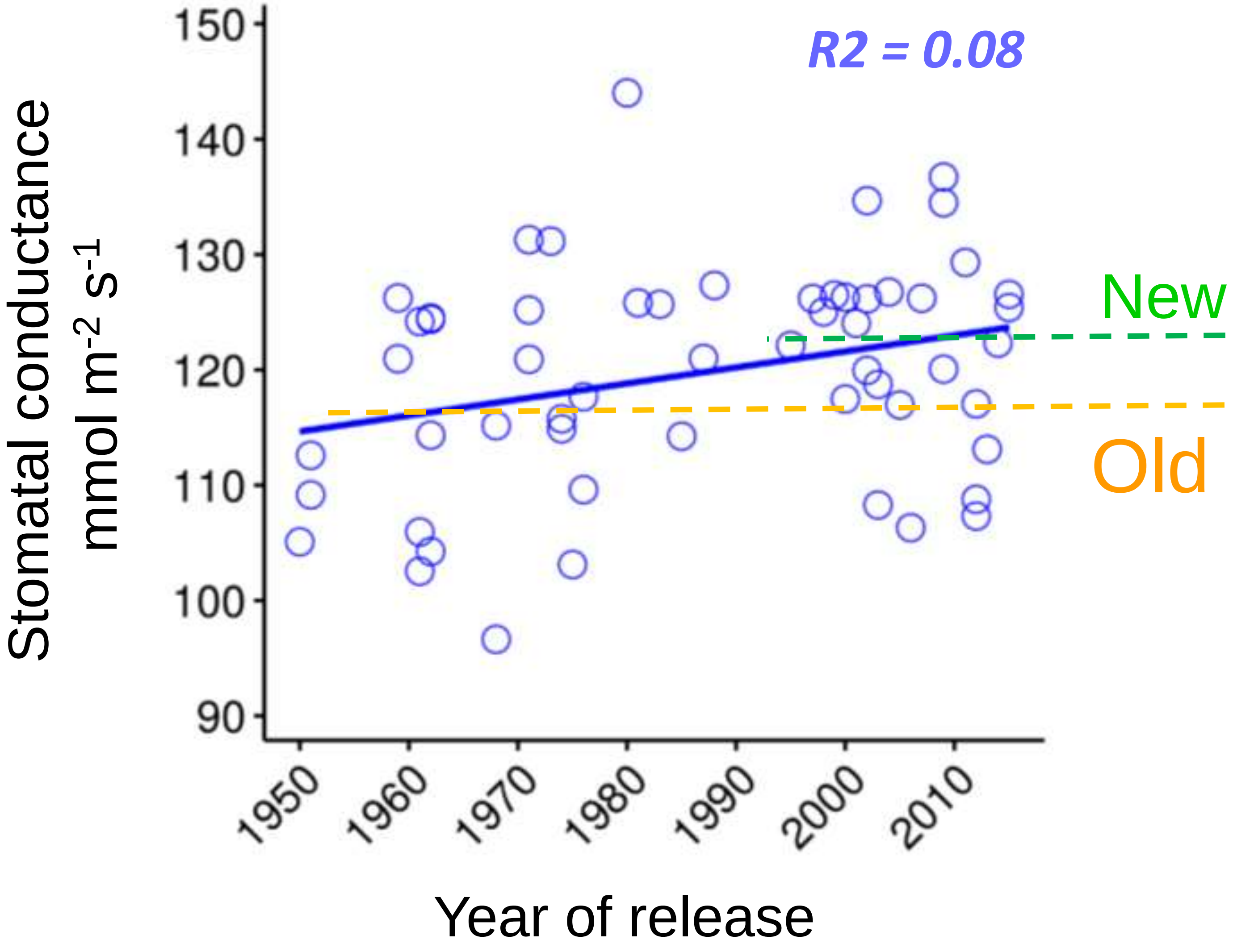
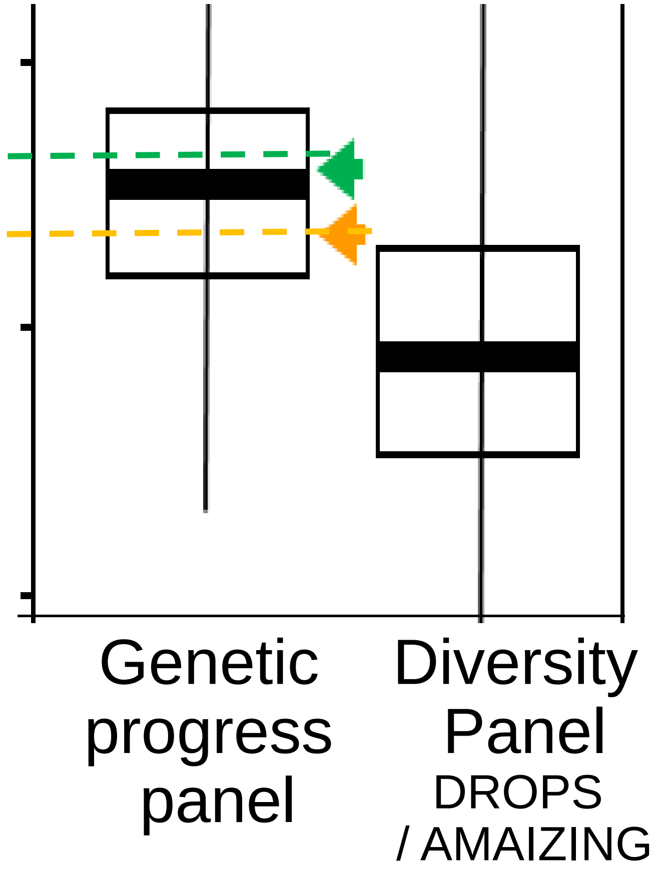




In spite of a large genetic variation and heritability in maize



Ll Cabrera

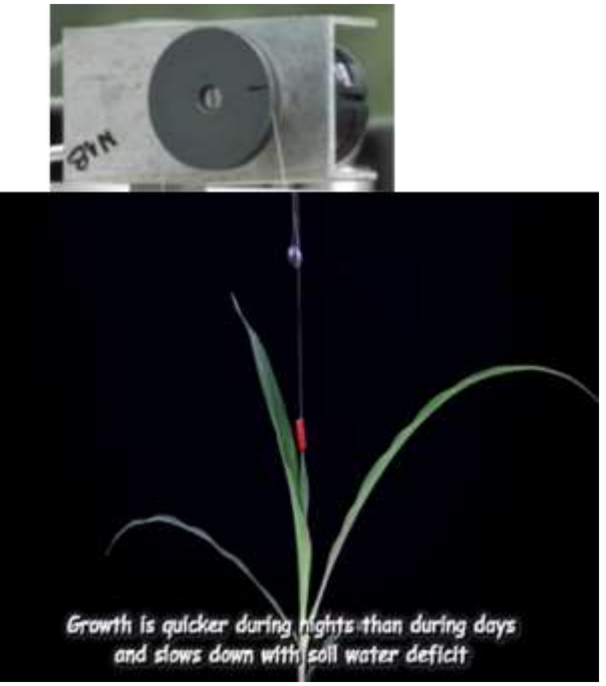
N Abou Amra Spencer

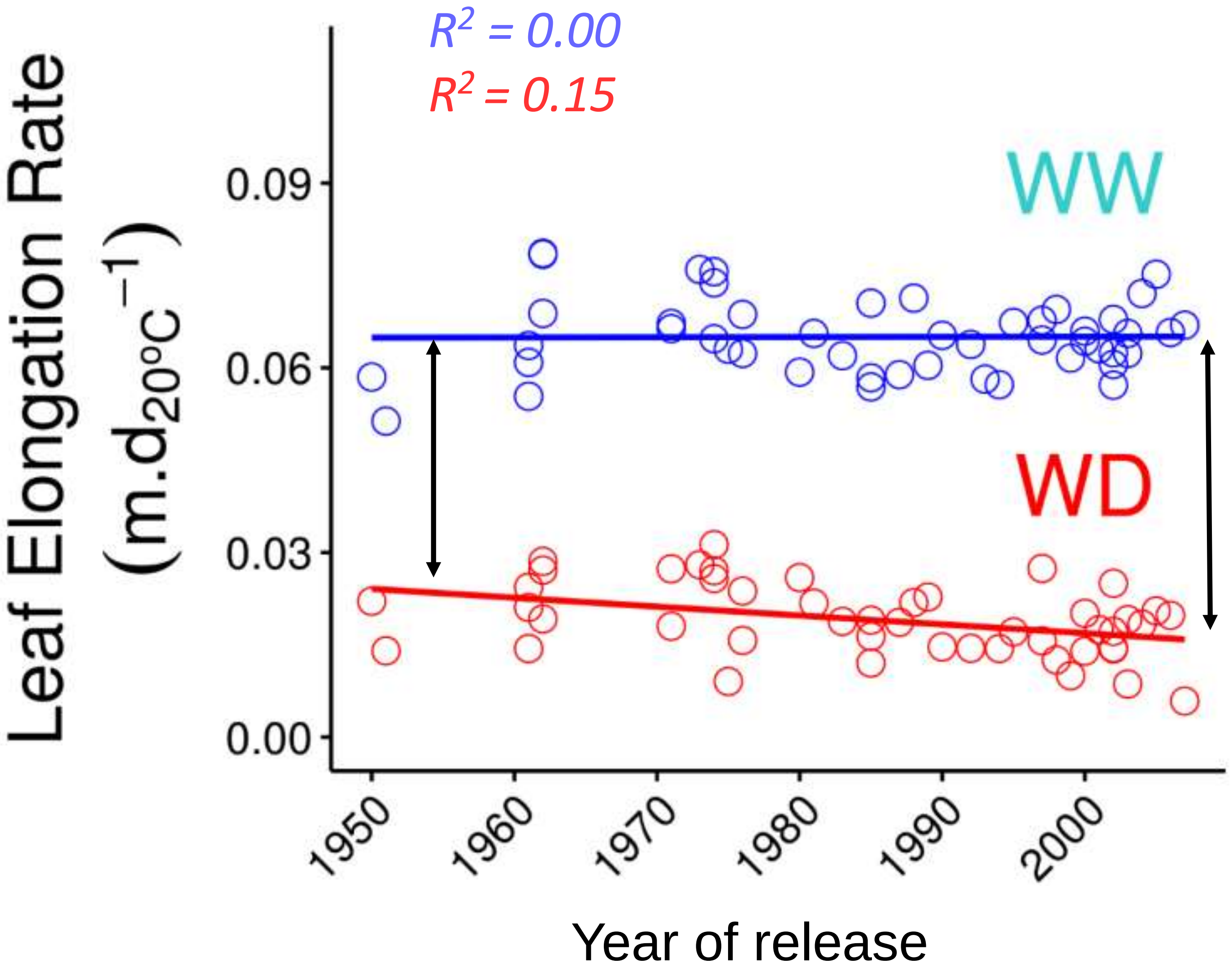
S. Alvarez Prado

Welcker et al 2022, Nature Communications

Genetic progress in maize, 1950 – 2010 Physiological adaptive processes

BUT leaf growth rate and its sensitivity to water deficit essentially unchanged





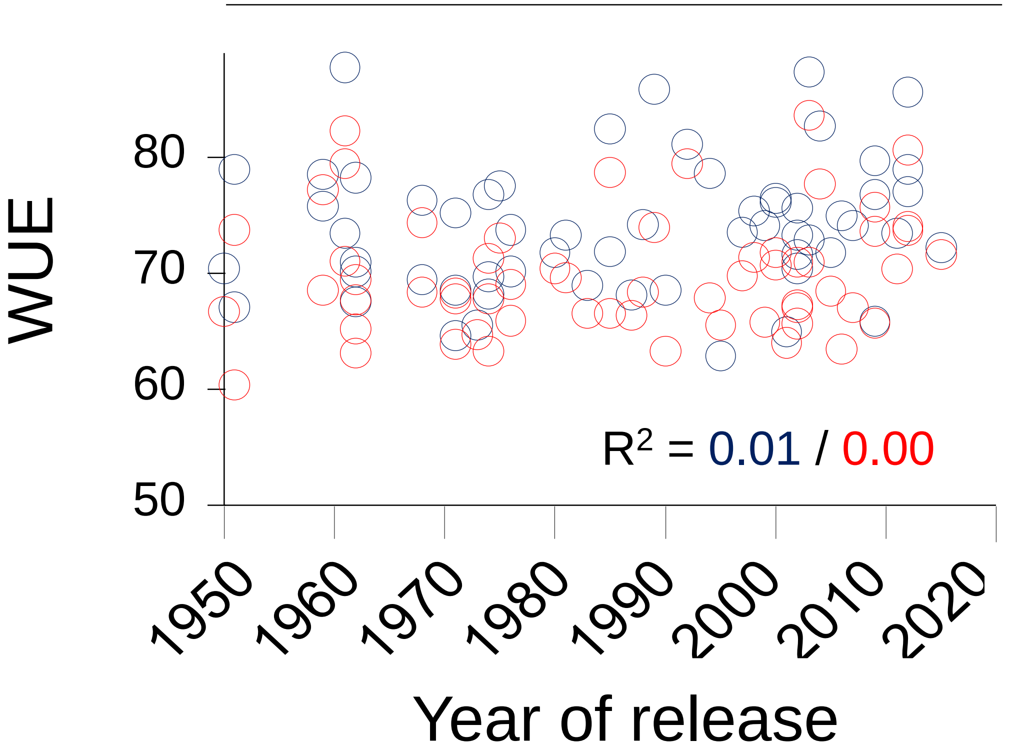

C. Welcker


R Chapuis

Welcker et al 2022, Nature Communications

Genetic progress in maize, 1950 – 2010 Physiological adaptive processes

Water use efficiency essentially unchanged



Welcker et al 2022, Nature Communications

Yield QTLs with conditional effects, a reservoir of alleles ?

Overall, genetic progress linked to phenology and architecture

A room for "unstable" QTLs in yield ?

Physiological adaptive processes not affected
In spite of large genetic variability and heritability

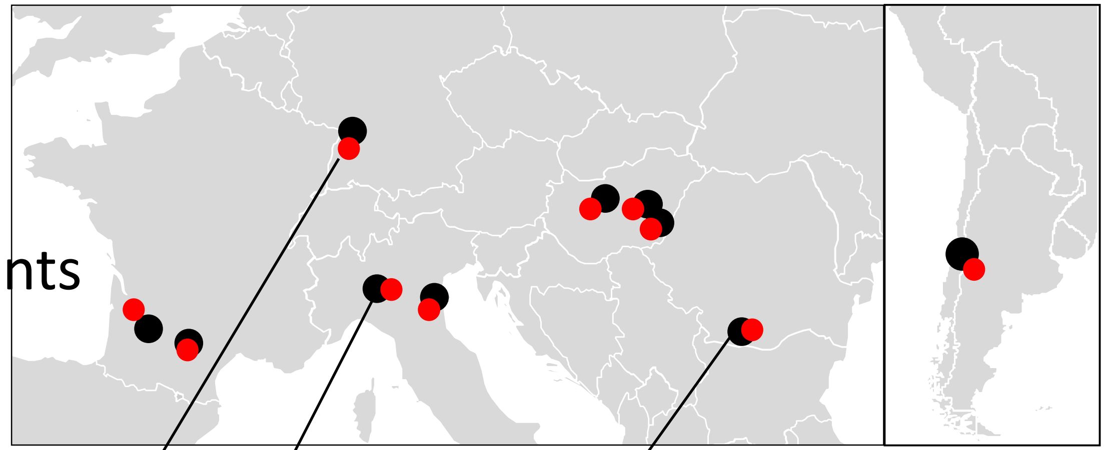
Parallel progress of traits and yield

Only "constitutive" traits with low GxE were improved

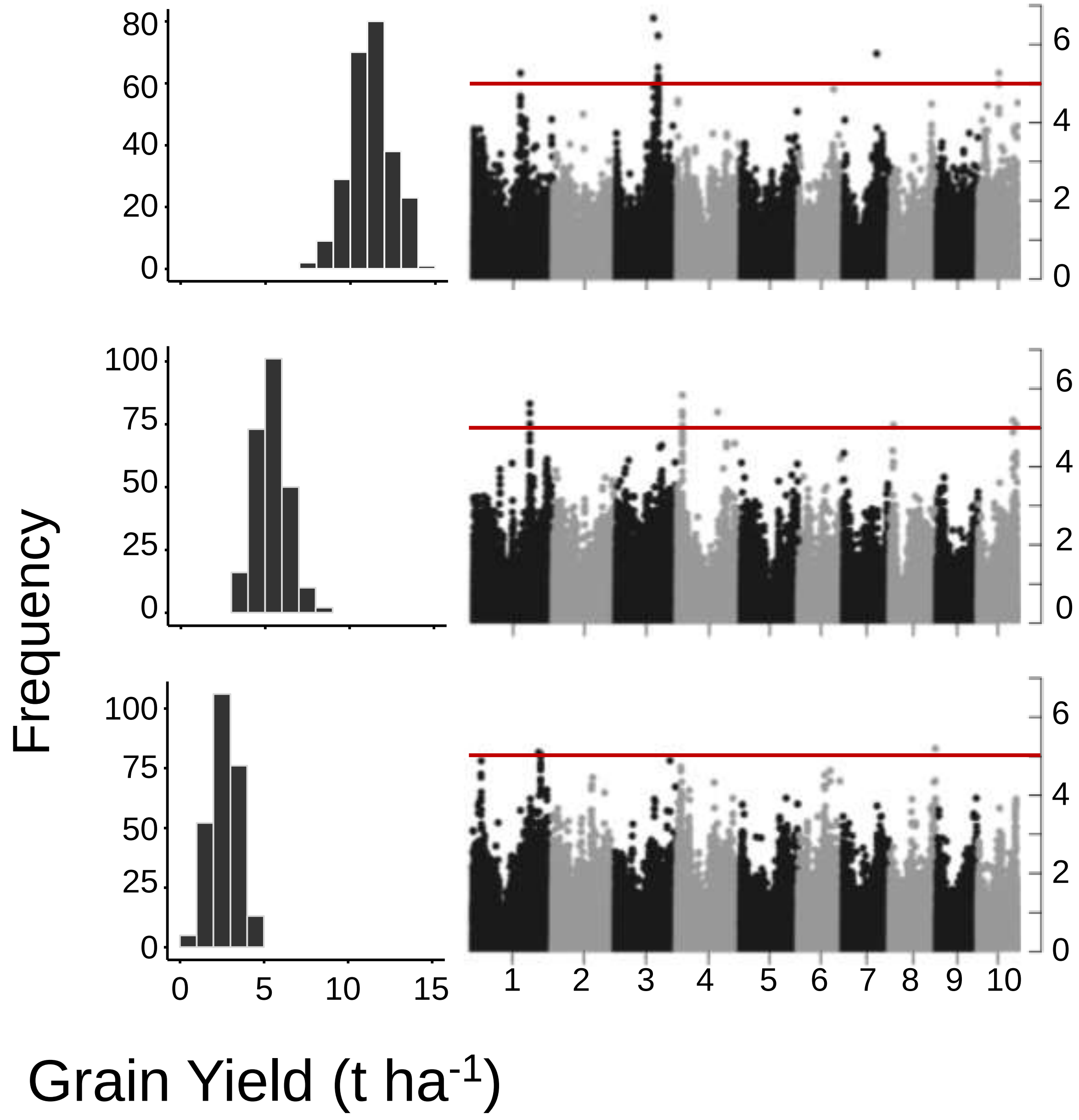
Yield QTLs with conditional effects, a reservoir of alleles ?

252 genotypes
950k polymorphic markers
Yield variations from 5 to 12 T ha^{-1}

16 fields
x
2 years
x
2 W treatments



490 significant SNPs, few in common



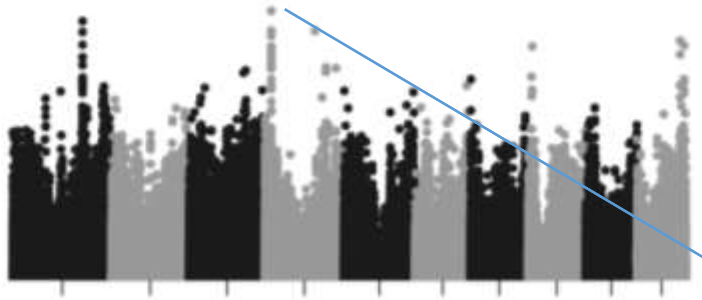
WW, cool

WW, hot

WD, hot

Millet *et al.2016* Plant Phys

Yield QTLs with conditional effects, a reservoir of alleles ?



Allelic effects 1 QTL. each square, one scenario

16 fields
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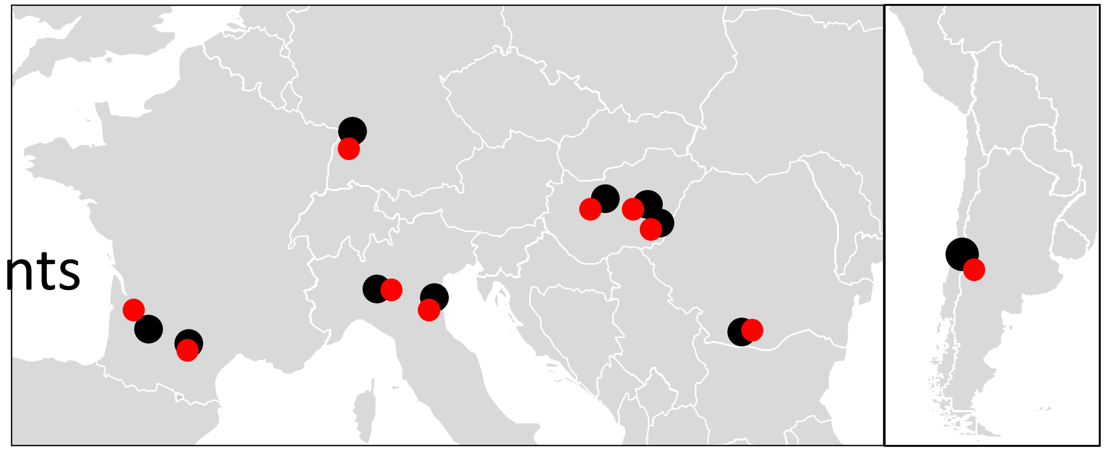
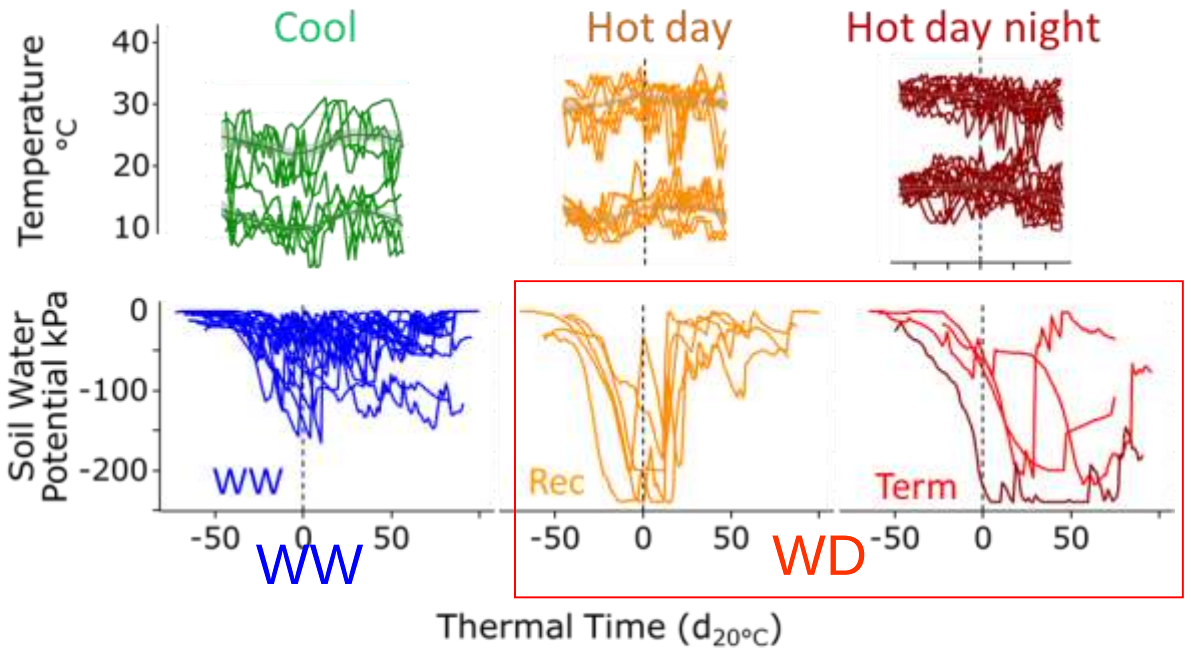
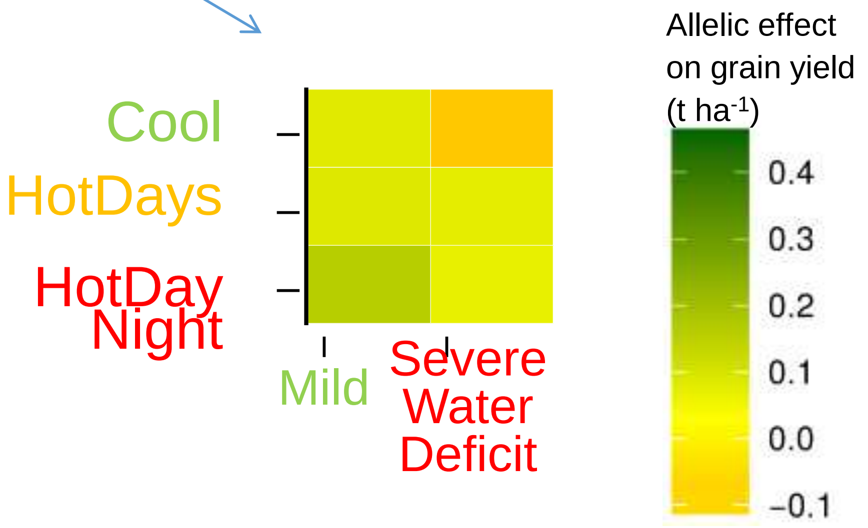
2 years
x
2 W treatments



Coll van Eeuwijk
Charcosset





Millet *et al. 2016* Plant Phys

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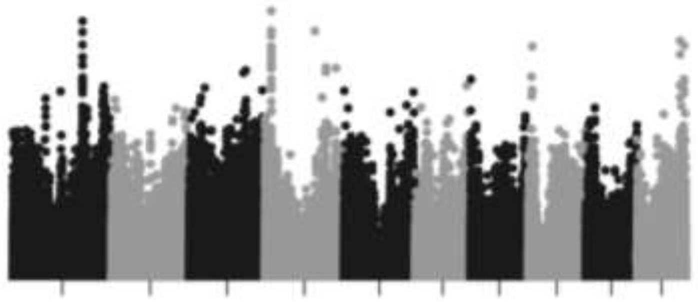

16 fields
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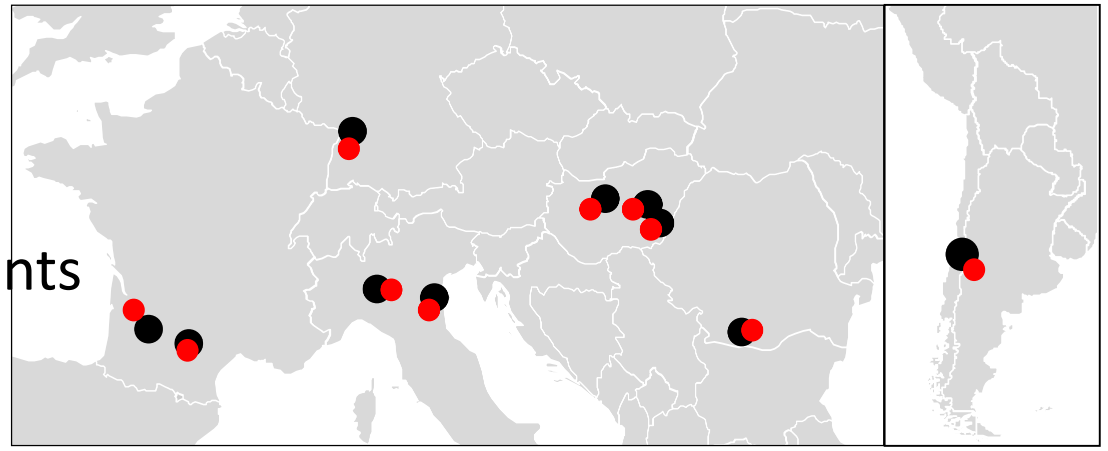
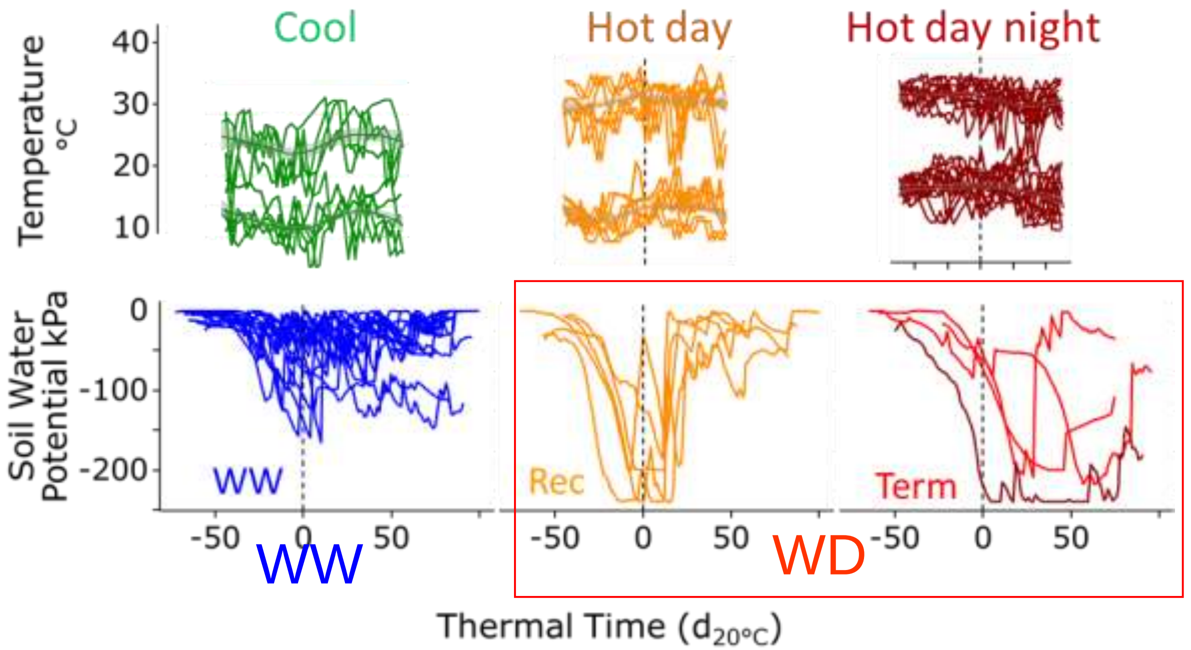
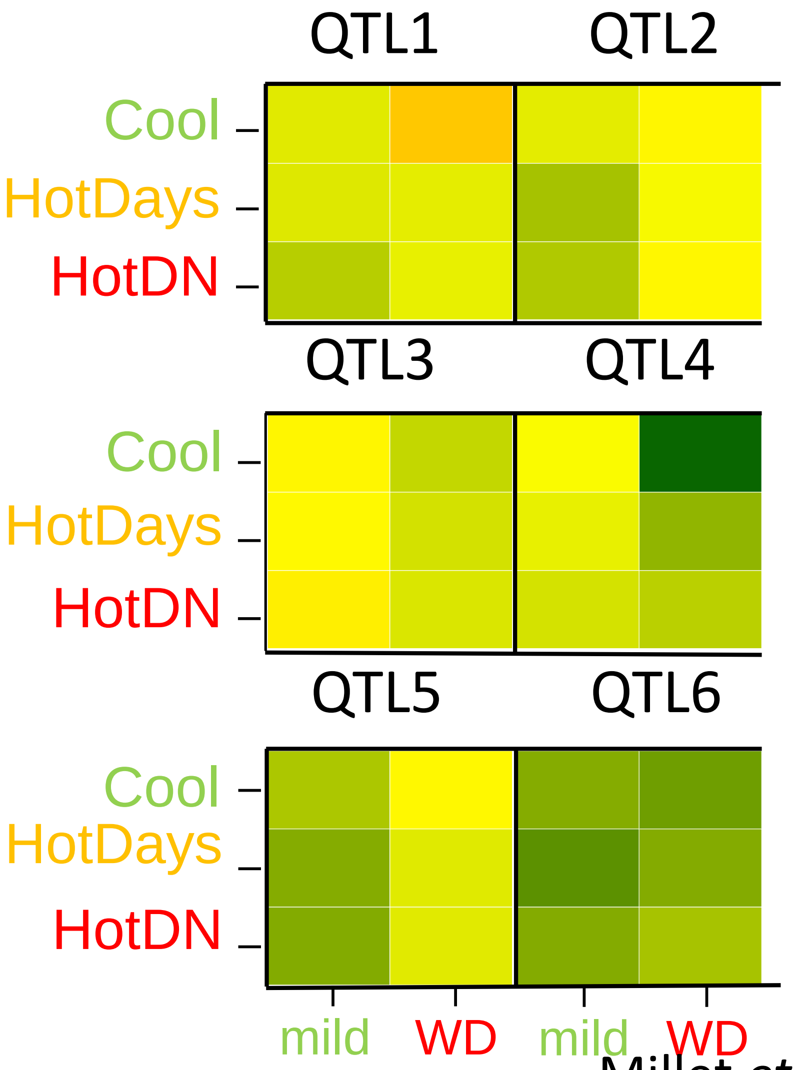
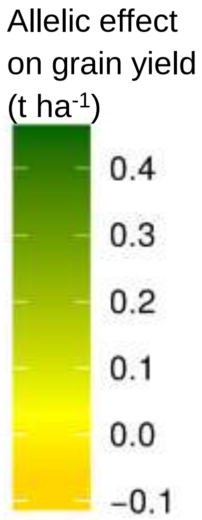


Allelic effects 6 QTL. each square, one scenario

Coll van Eeuwijk
Charcosset



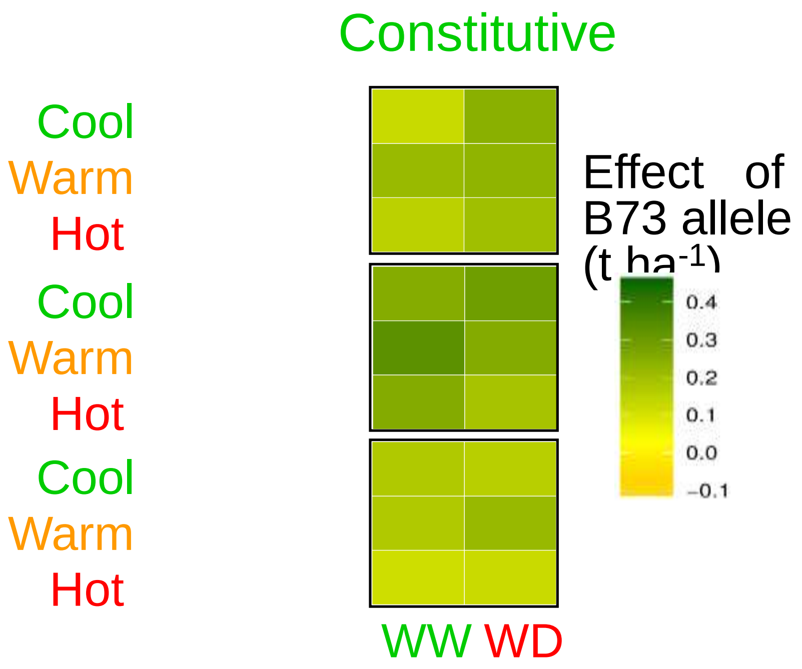




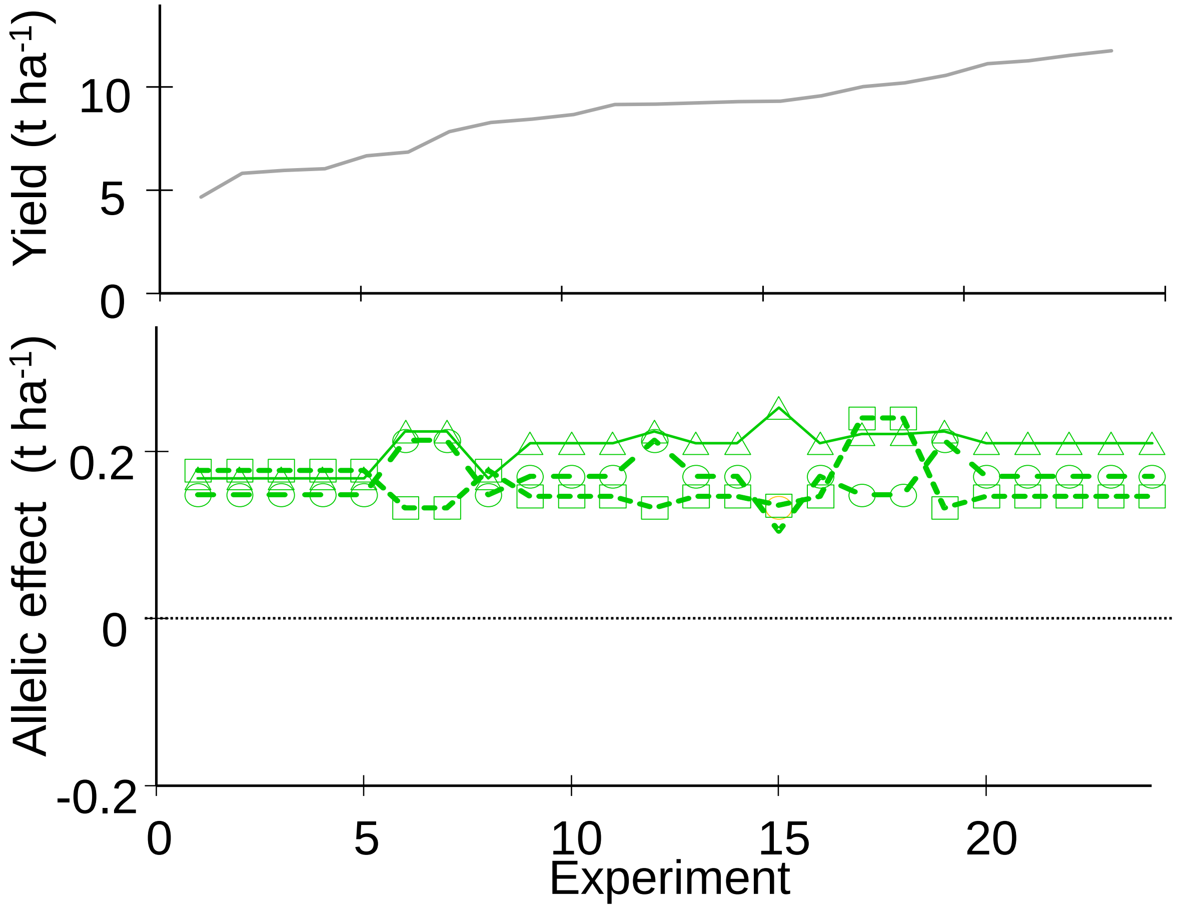
Millet *et al. 2016* Plant Phys

Yield QTLs with conditional effects, a reservoir of alleles ?

Hypothesis: when selecting for yield, one only “fishes” alleles with consistently + effects



Stable, constitutive QTLs (architecture, phenology)
Improve yield in all experiments:
Good genetic correlation of traits with yield



Welcker et al 2022, Nature Communications

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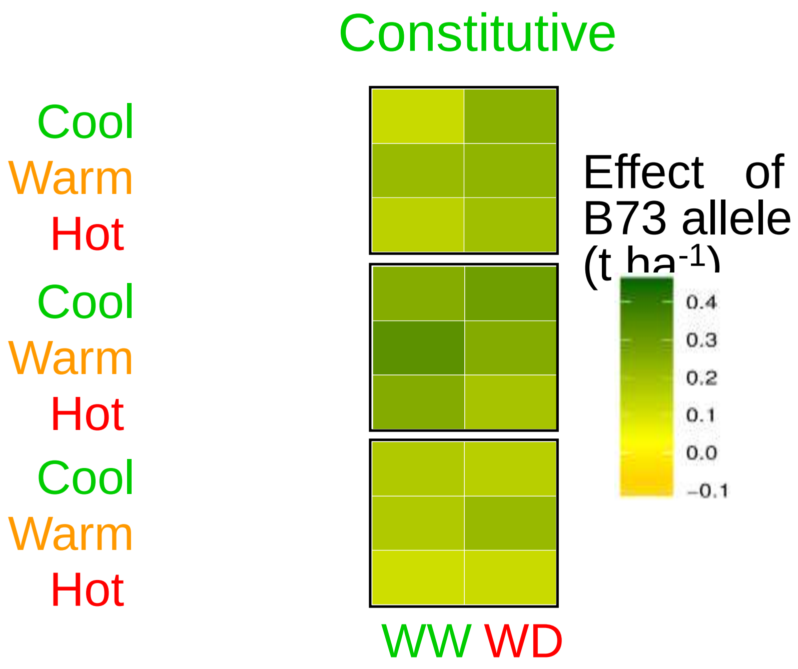
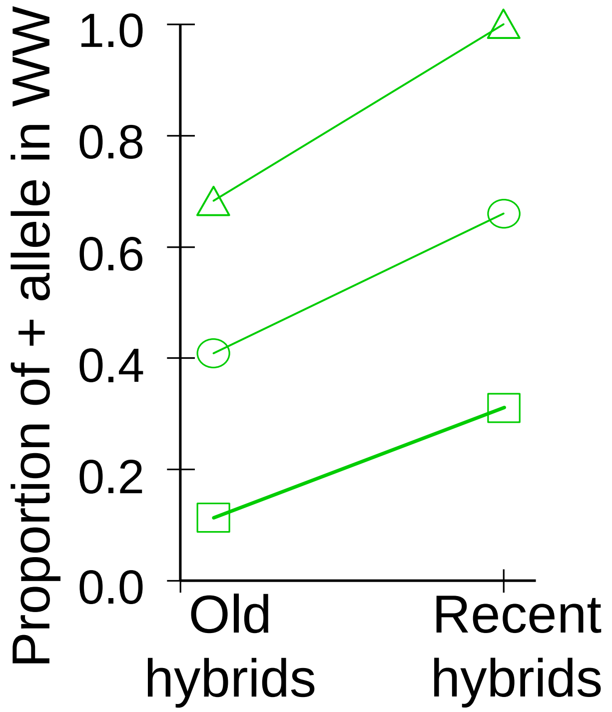
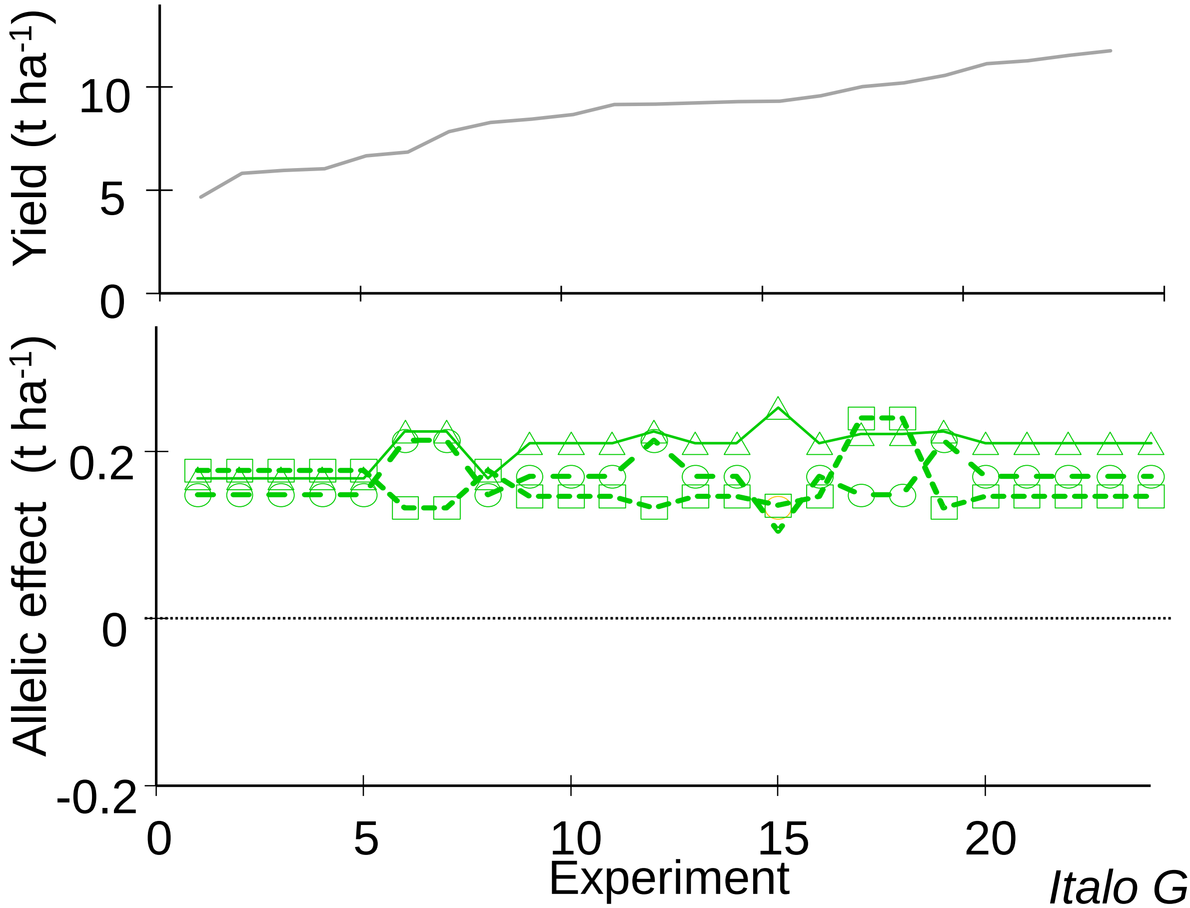
Increased proportion of + alleles (WW) in recent hybrids







Welcker et al 2022, Nature Communications

Italo Granato

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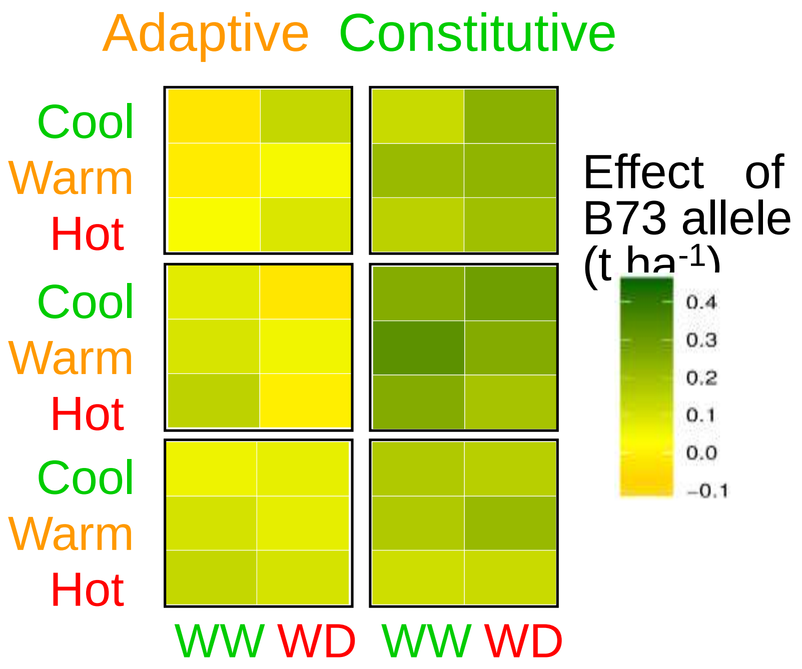

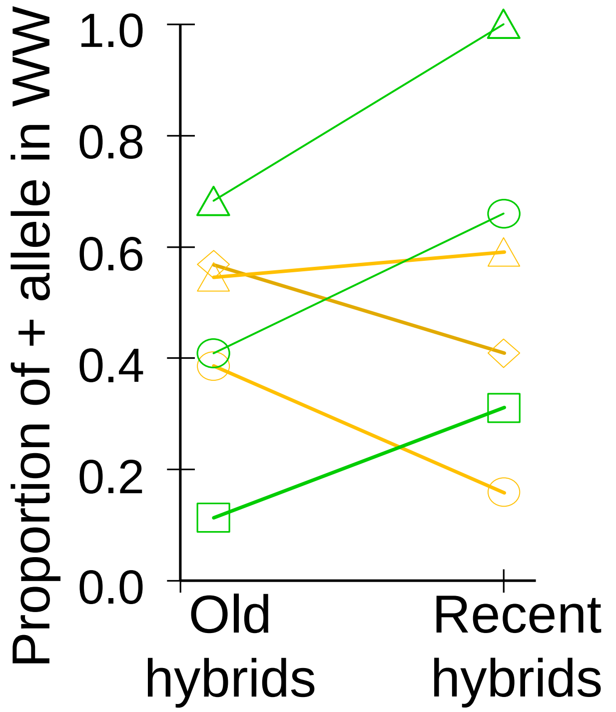

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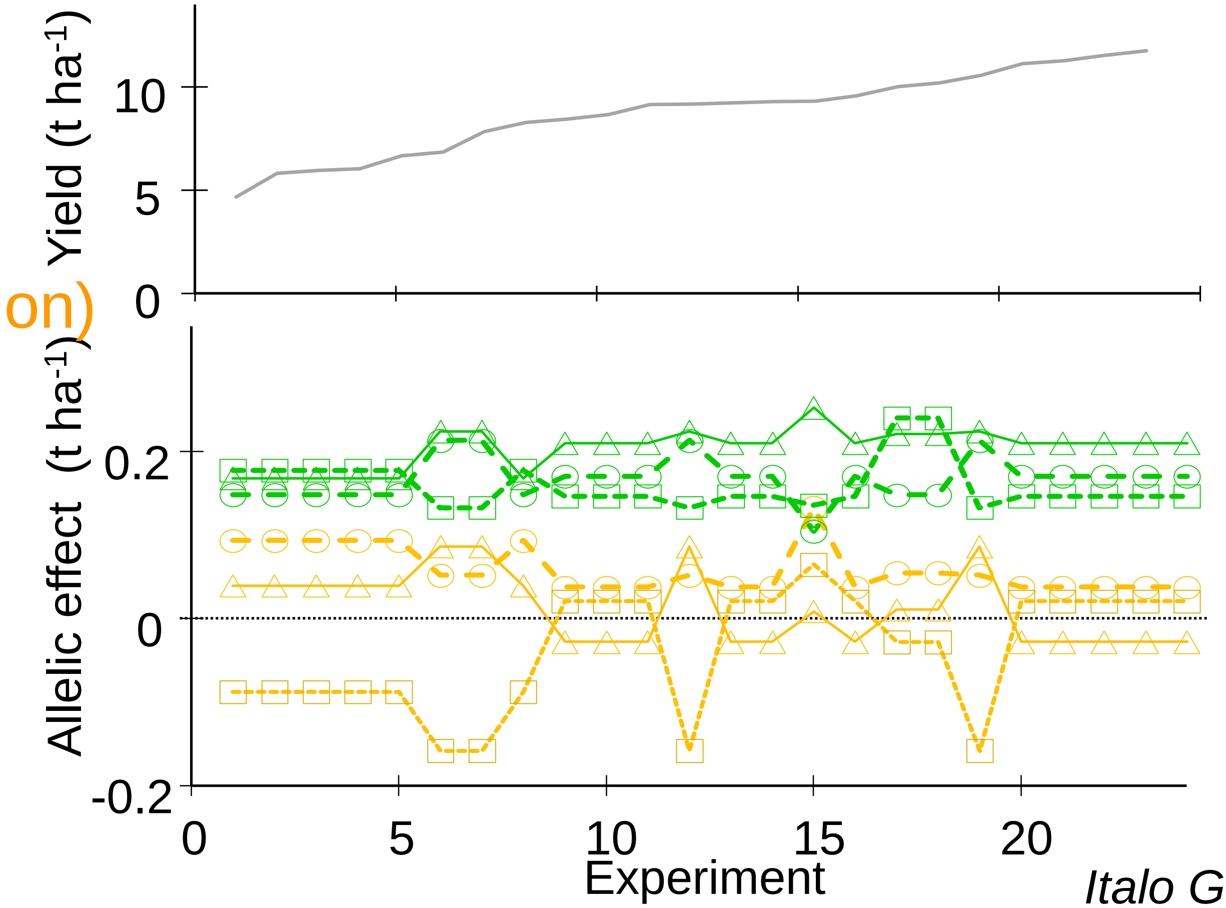


Unstable, adaptive QTLs (stomatal conductance, transpiration)
Clear effect in some conditions, other not:
Genetic correlation of traits with yield is good but unstable

Proportion of + alleles (WW) did not increase

Welcker et al 2022, Nature Communications

Italo Granato

Yield QTLs with conditional effects, a reservoir of alleles ?

- **“Unstable” QTLs for yield represent the vast majority of yield QTLs**

- **BUT breeding programs based on yield selected**

  constitutive traits such as phenology, reproductive development and architecture, similarly in all tested environments

  Did not improve physiological adaptive traits

Which space for phenotyping ?

Phenotyping: what to do ?

- **Demand from breeders:** plant number, prediction of harvest ?
  Yes for methodology, perhaps in the domain of SMEs for meeting the demand

- **Comment the genetic progress ?**
  Useful, not sufficient

- **Identify new opportunities?**

To what extent traits in a platform translate to field ?

By default they don’t !
The best way to spend public money without return is to measure yield in a platform…

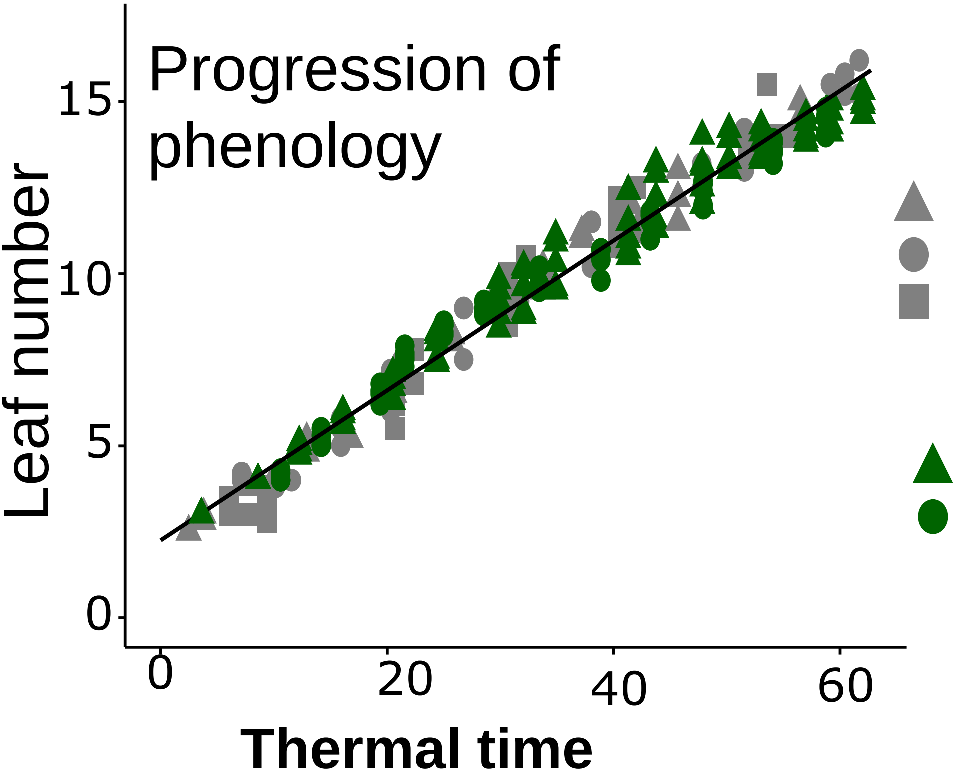
But yes, they can, provided that precautions are taken

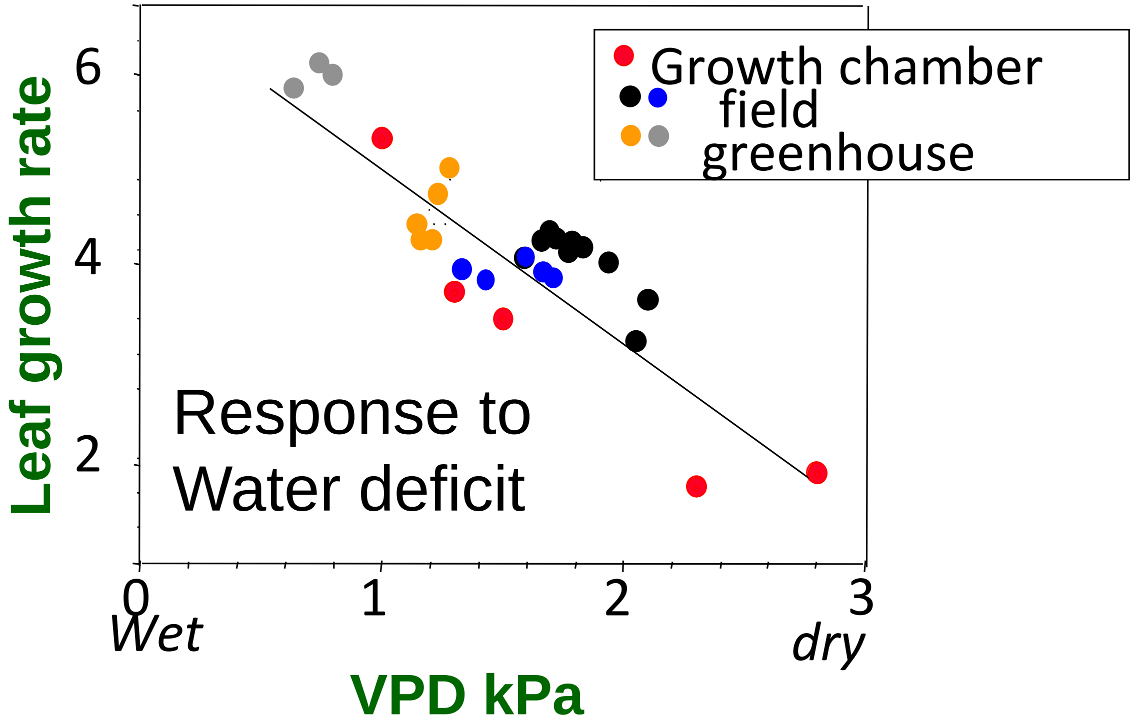
To what extent traits in a platform translate to field ? phenology and responses

In some cases, platforms can represent field, after some effort

One can measure genotype-specific traits in platforms

Traits, *1 genotype*





S. Alvarez Prado

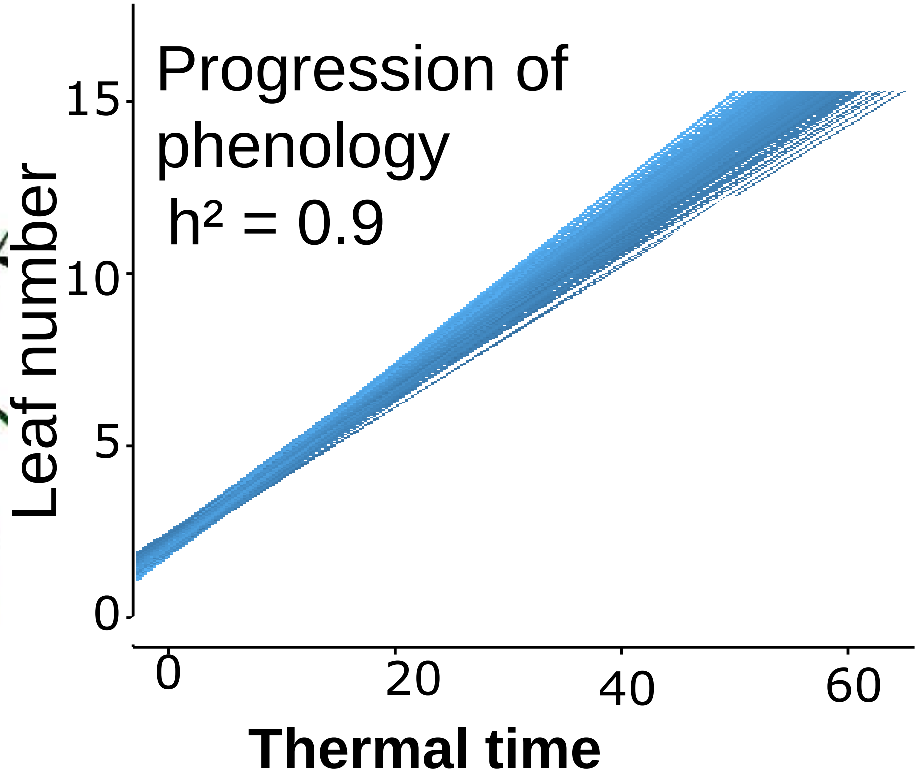
Ll Cabrera

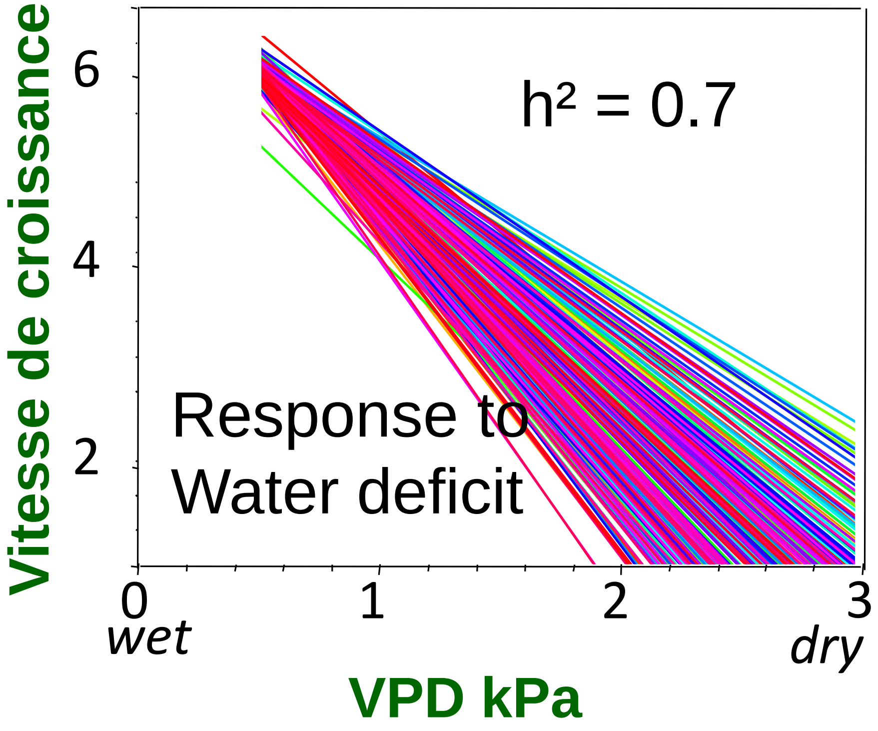
To what extent traits in a platform translate to field ? phenology and responses

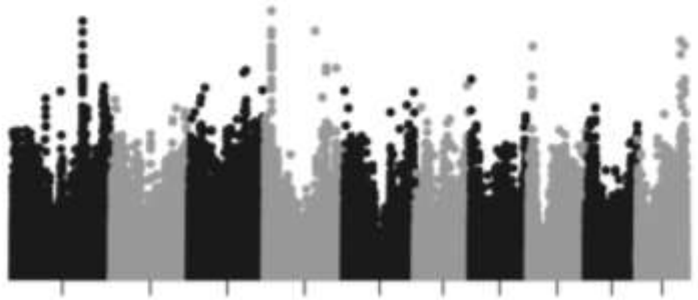
In some cases, platforms can represent field, after some effort

One can measure genotype-specific traits in platforms, traits are heritable

Traits, *250 genotype*







Genetic dissection

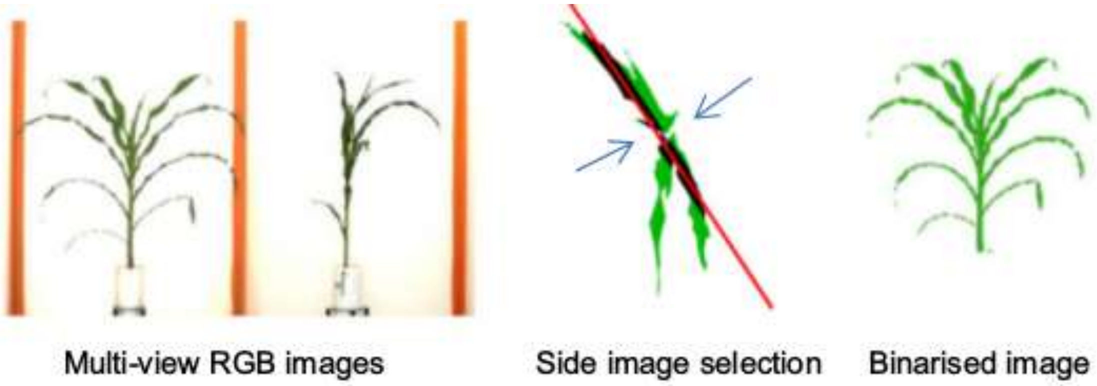
S. Alvarez Prado

Ll Cabrera

To what extent traits in a platform translate to field ? Plant architecture

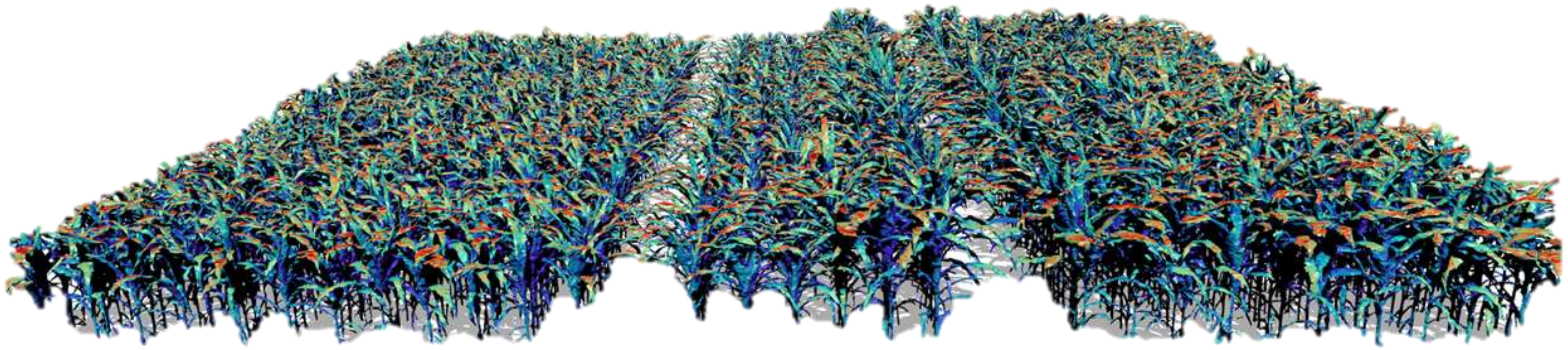
Light interception and RUE from Imaging and modelling

Imaging



250 hybrids

Reconstruction



Perez et al. 2019 PCE
Chen et al 2019 J .Exp Bot

Tardieu et al 2017 Current Biol


R. Perez

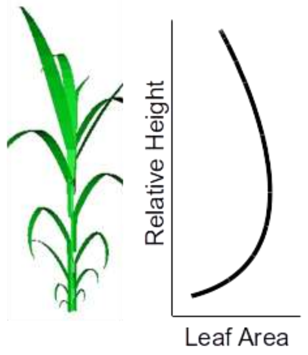

C Fournier

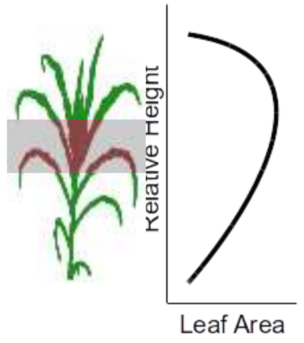

Ll Cabrera

To what extent traits in a platform translate to field ? Plant architecture

In some cases, platforms can represent field, after some effort

One can measure genotype-specific traits in platforms





rh$_{PAD}$ (% total height)

R. Perez

C Fournier

Ll Cabrera

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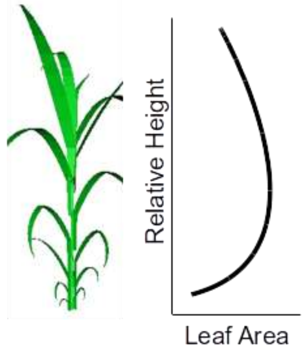
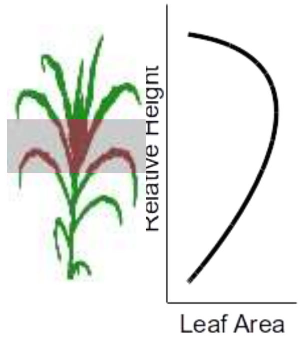
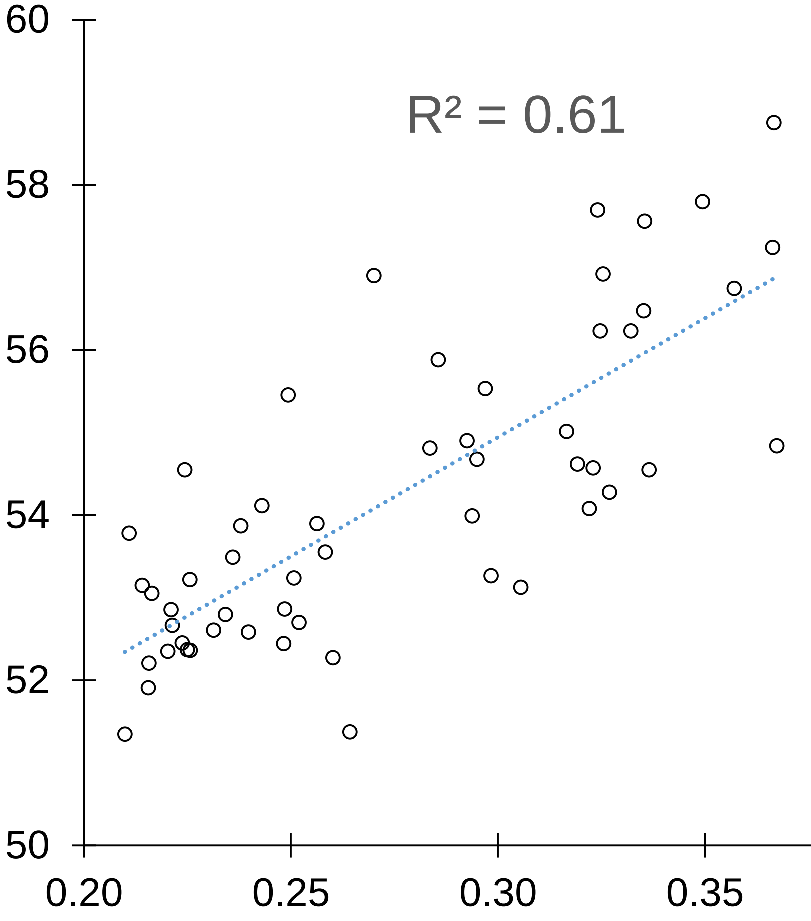




rh$_{PAD}$ (% total height)

Field (Drone)
Model inversion
(Prosail)



Platform (3D imaging)

C. Welcker

R Chapuis

R. Perez

C Fournier

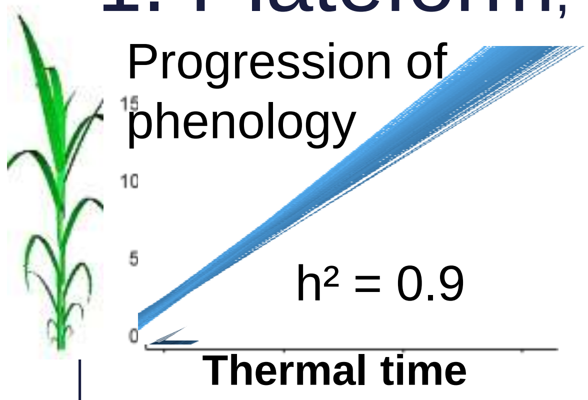
Ll Cabrera

New opportunity: Combining phenomics, modelling and genomic prediction for climate change

Genomic prediction of maize yield across European environmental scenarios

Millet et al 2019 Nature Genetics

1. Plateform, 250 geno



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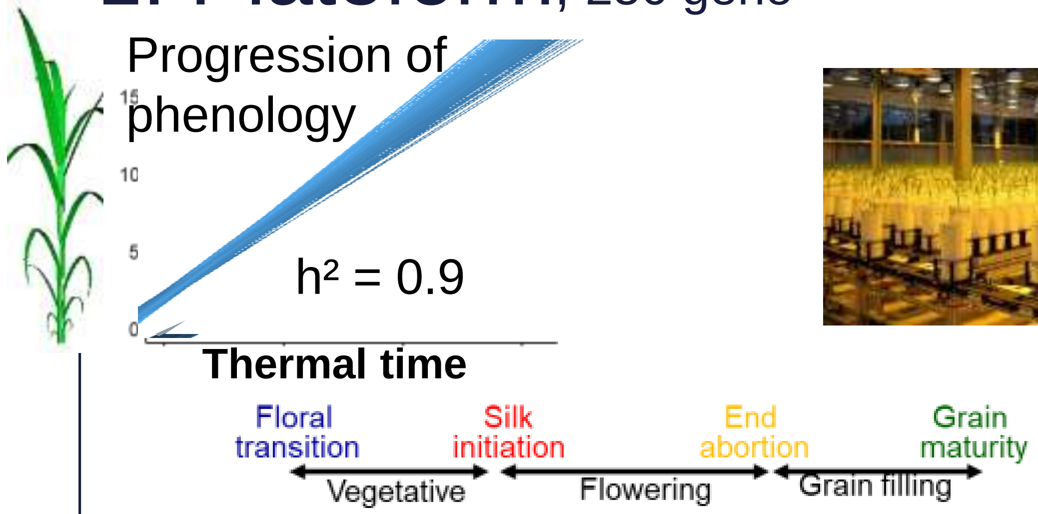
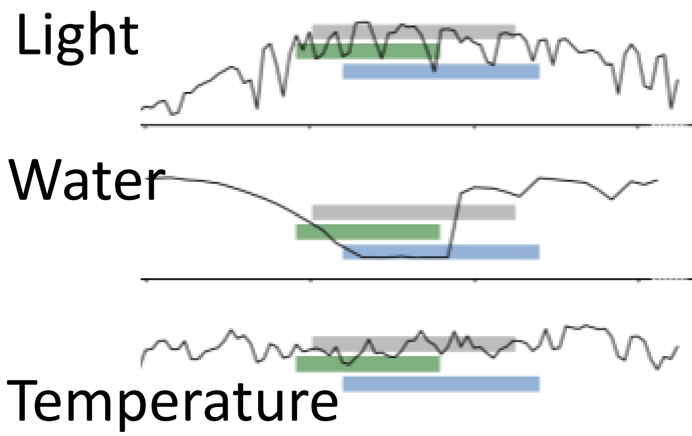
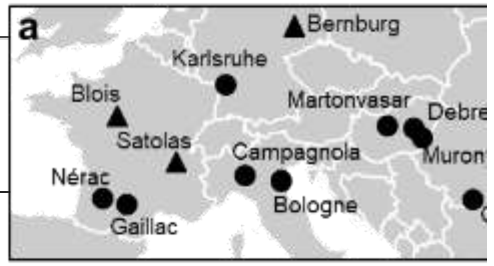


2. Field, Conditions felt by 250 genotypes in 25 fields





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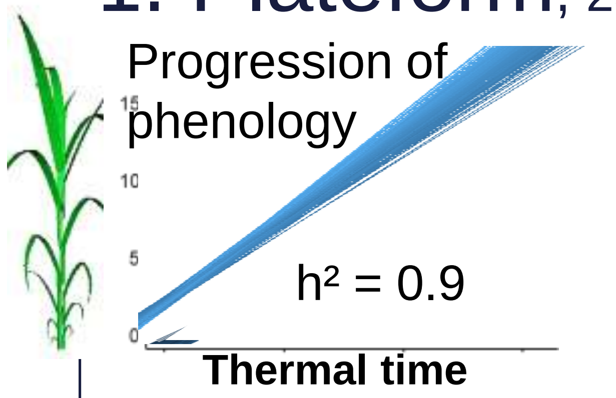

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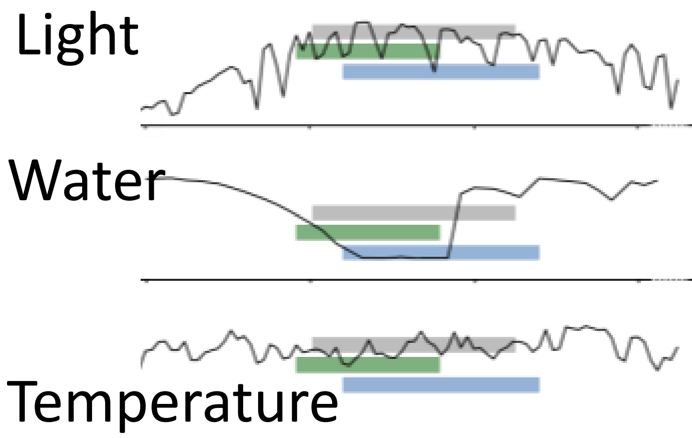
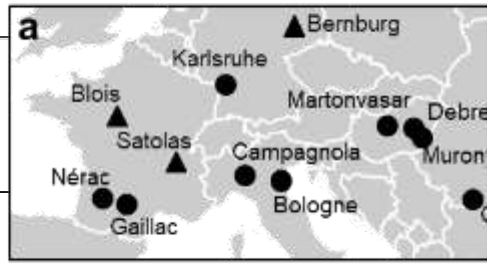
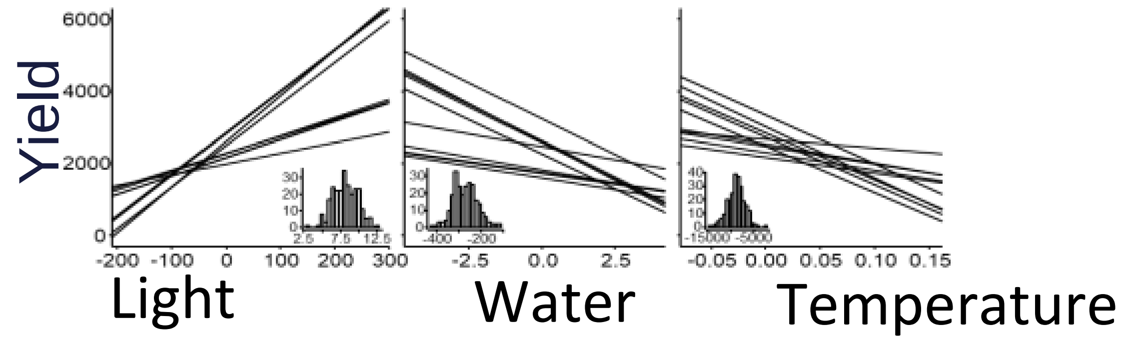




3. Response curves, 250 geno



4. Genomic prediction, 250 geno

$$GY_{ij} = (\mu + e_j + g_i + \sum_{l=1}^{s} \beta_{l,i}\, cov_{l,i,j}) \times GW_i$$

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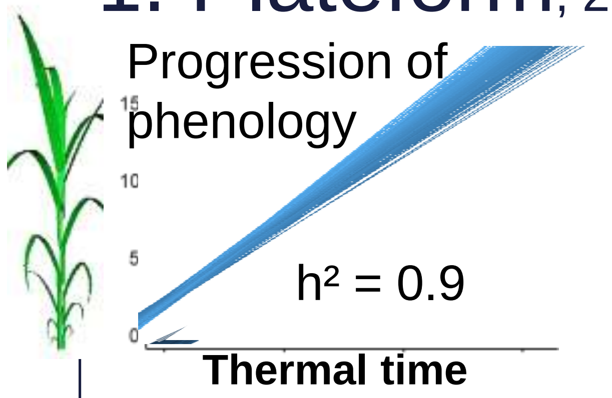

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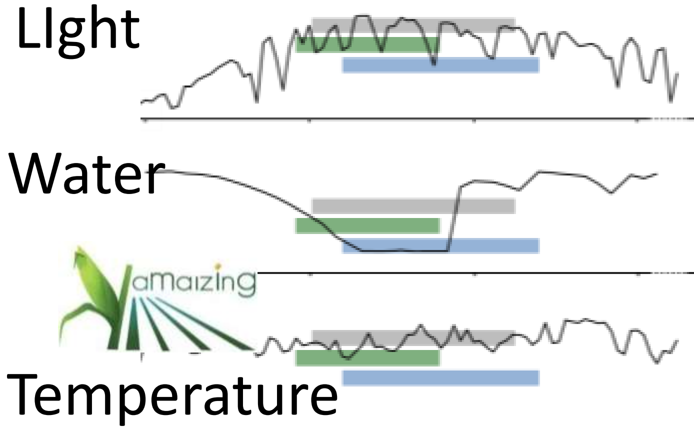

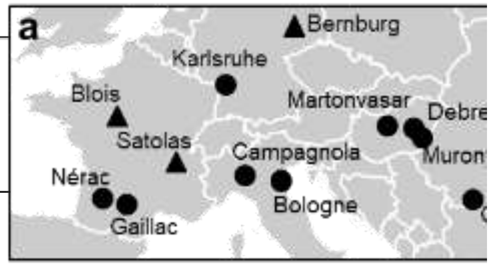

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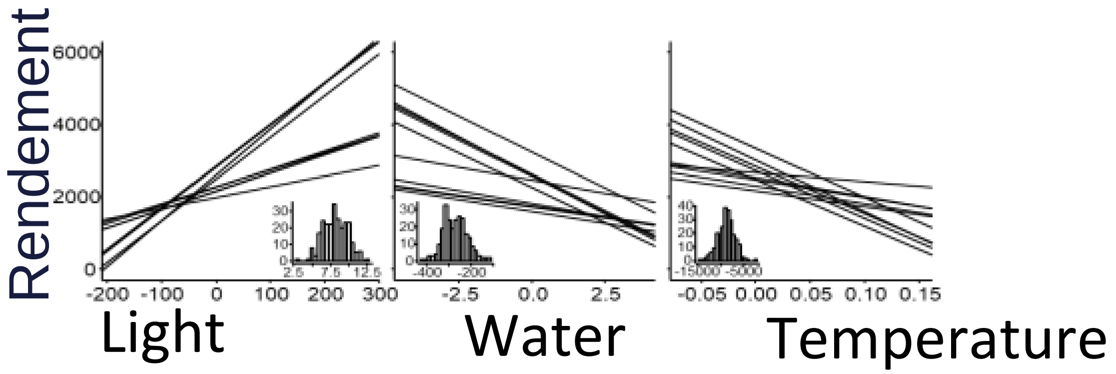

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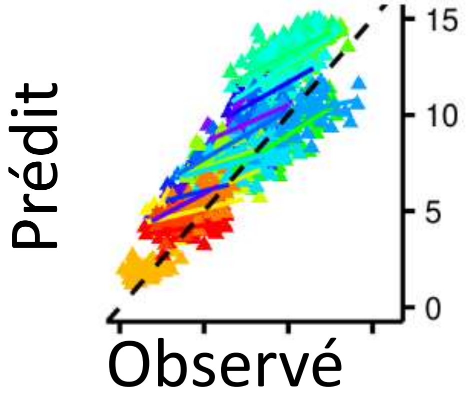
$$GY_{ij} = (\mu + e_j + g_i + \sum_{l=1}^{s} \beta_{l,i}\, cov_{l,i,j}) \times GW_i$$

5. Test, New geno in new fields

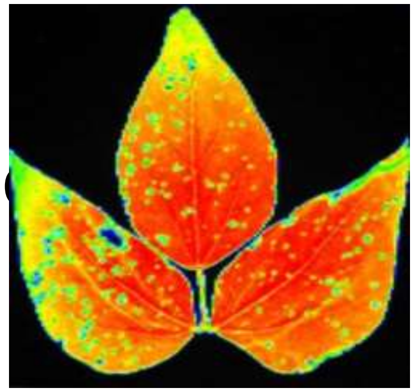


Which geno (1000s) in which fields (1000s)

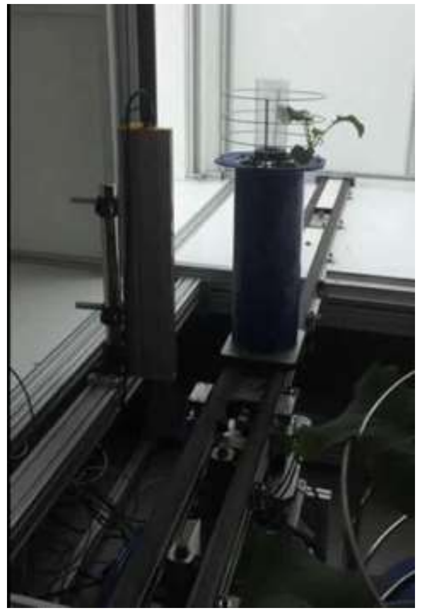
New opportunities: Agroecology

Quantify the interactions between genotype and microbiome

Early detection of diseases, genotypic differenc
(multisprectral imaging
  deep learning, genetic analyses)



Symbiosis
Deep learning, genetic analyses



New opportunities: Agroecology

Complex canopies: avoid diseases, more resilient to abiotic stresses

Recognize species in a complex canopy :
- Diagnostic and modelling : what was actually achieved,
- Perspective for digital agriculture

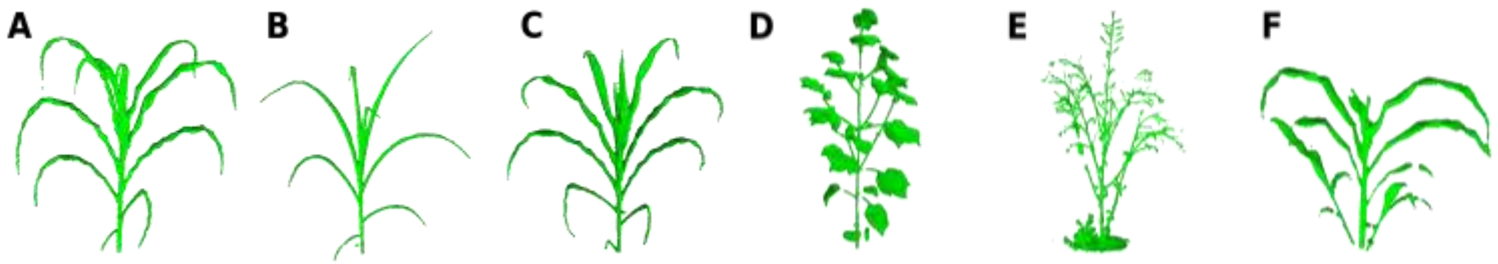
Imaging + deep learning

Identification of both species

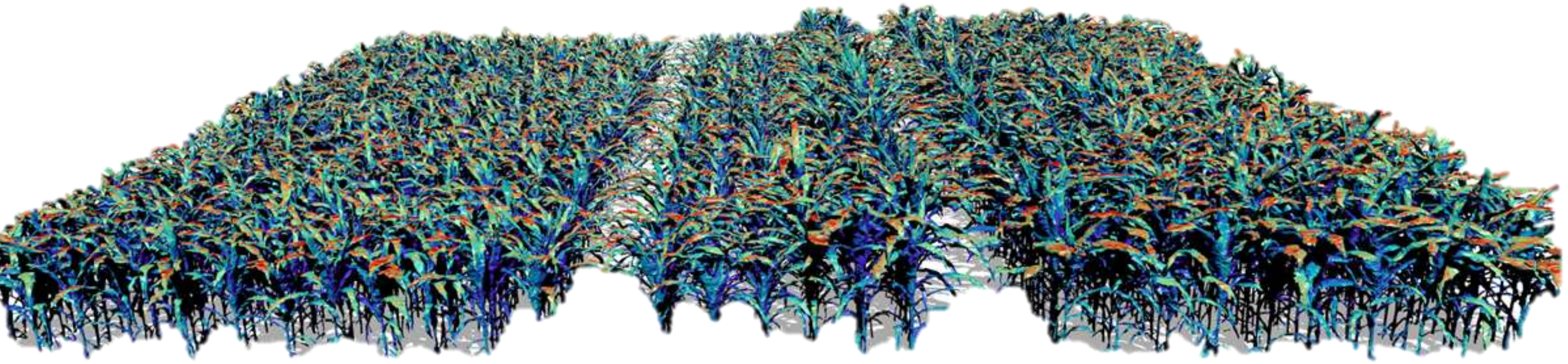
Benoît De Solan

New opportunities: Agroecology

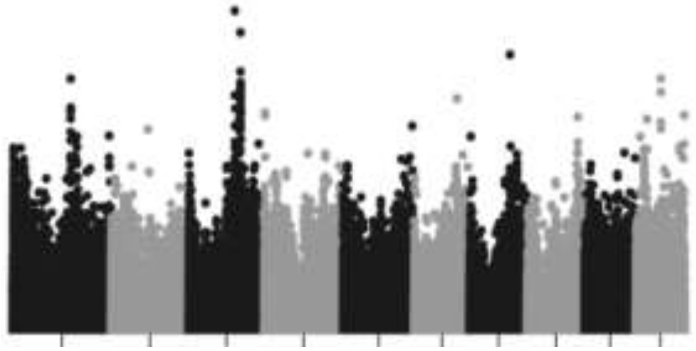
Complex canopies simulating effects from individual plants



Characterization of individual plants
of each species/genotype



100s virtual canopies that include these plants
Modélling the circulation of spores, intercepted light
Yield. Optimization



Genetic analysis
Which alleles for optimizing te association ?

C Fournier

Ll Cabrera

Conclusion:

Perspectives for the contribution to breeding are not where we expected

- **Phenotyping in breeding programmes : needs new breeding approaches,probably necessary with climate change**

  to be developped with breeders

- **Agro ecology**

  Complex canopies, early detection of diseases

New methods to be developped

- **The debate indoor vs field probably not relevant**

A platform does not represent THE field, but a field does not represent another field
Phenotyping : explicit and model which genotypes where

- **Association phenomics – modelling – deep learning – genomic prediction**

- **Data management will be central**

Acknowledgements

PHENOME FRANCE EMPHASIS

amaizing

DROPS

Field experiments

KWS
T. Presterl

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A. Murigneux

syngenta
N. Ranc

RAGT, Euralis
MaisAdour

biogemma
S. Praud

Genetic analyses

INRAE science for people, life & earth
Moulon,
A Charcosset
S Nicolas

Wageningen
F van Eeuwijk
Willem Kruijer

lepse Montpellier

N Abou Amra
Spencer

Italo Granato

E. Millet

Platform experiments, modelling

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lepse Montpellier

C Welcker

B. Parent

S. Alvarez
Prado

Ll Cabrera

O. Turc